



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ST. GEORGE-HYSLOP, PETER H
ROMMENS, JOHANNA M
FRASER, PAUL E
- (ii) TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
- (iii) NUMBER OF SEQUENCES: 160
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Testa, Hurwitz & Thibeault
 - (B) STREET: High Street Tower - 125 High Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/509,359
 - (B) FILING DATE: 31-JUL-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Twomey, Michael J
 - (B) REGISTRATION NUMBER: 38349
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 248-7362
 - (B) TELEFAX: (617) 248-7100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGGGACAGGC AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG	60
GAAGGAACCT GAGCTACGAG CCGCGGCGGC AGCGGGGCGG CGGGGNAAGC GTATACCTAA	120
TCTGGGAGCC TGCAAGTGAC AACAGCCTTT GCGGTCTTA GACAGCTTGG CCTGGAGGAG	180
AACACATGAA AGAAAGAACCC TCAAGAGGCT TTGTTTCTG TGAAACAGTA TTTCTATACA	240
GTTGCTCCAA TGACAGAGTT ACCTGCACCG TTGTCCTACT TCCAGAATGC ACAGATGTCT	300

GAGGACAACC ACCTGAGCAA TACTGTACGT AGCCAGAATG ACAATAGAGA ACGGCAGGAG 360
CACAAACGACA GACGGAGCCT TGGCCACCCCT GAGCCATTAT CTAATGGACG ACCCCAGGGT 420
AACTCCCGGC AGGTGGTGGA GCAAGATGAG GAAGAAGATG AGGAGCTGAC ATTGAAATAT 480
GGCGCCAAGC ATGTGATCAT GCTCTTGTC CCTGTGACTC TCTGCATGGT GGTGGTCGTG 540
GCTACCATTA AGTCAGTCAG CTTTATACC CGGAAGGATG GGCAGCTAAT CTATACCCCA 600
TTCACAGAAG ATACCGAGAC TGTGGGCCAG AGAGCCCTGC ACTCAATTCT GAATGCTGCC 660
ATCATGATCA GTGTCATTGT TGTCACTGACT ATCCTCCTGG TGGTTCTGTA TAAATACAGG 720
TGCTATAAGG TCATCCATGC CTGGCTTATT ATATCATCTC TATTGTTGCT GTTCTTTTT 780
TCATTCAATT ACTTGGGGGA AGTGTAAACCTATAACG TTGCTGTGG CTACATTACT 840
GTGCACTCC TGATCTGGAA TTTGGGTGTG GTGGGAATGA TTTCCATTCA CTGGAAAGGT 900
CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCCTCATGGC CCTGGTGT 960
ATCAAGTACC TCCCTGAATG GACTGCGTGG CTCATCTTGG CTGTGATTTC AGTATATGAT 1020
TTAGTGGCTG TTTGTGTCC GAAAGGTCCA CTTCGTATGC TGGTTGAAAC AGCTCAGGAG 1080
AGAAATGAAA CGCTTTTCC AGCTCTCATT TACTCCTCAA CAATGGTGTG GTTGGTGAAT 1140
ATGGCAGAAG GAGACCCGGAA AGCTCAAAGG AGAGTATCCA AAAATTCCAA GTATAATGCA 1200
GAAAGCACAG AAAGGGAGTC ACAAGACACT GTTGCAGAGA ATGATGATGG CGGGTTCACT 1260
GAGGAATGGG AAGCCCAGAG GGACAGTCAT CTAGGGCCTC ATCGCTCTAC ACCTGAGTCA 1320
CGAGCTGCTG TCCAGGAAC TTCCAGCAGT ATCCTCGCTG GTGAAGACCC AGAGGAAAGG 1380
GGAGTAAAAC TTGGATTGGG AGATTCATT TTCTACAGTG TTCTGGTTGG TAAAGCCTCA 1440
GCAACAGCCA GTGGAGACTG GAACACAACC ATAGCCTGTT TCGTAGCCAT ATTAATTGGT 1500
TTGTGCCTTA CATTATTACT CCTGCCATT TTCAAGAAAG CATTGCCAGC TCTCCAATC 1560
TCCATCACCT TTGGGCTTGT TTTCTACTTT GCCACAGATT ATCTTGTACA GCCTTTATG 1620
GACCAATTAG CATTCCATCA ATTTTATATC TAGCATATTT GCGGTTAGAA TCCCATGGAT 1680
GTTTCTTCTT TGACTATAAC CAAATCTGGG GAGGACAAAG GTGATTTCC TGTGTCCACA 1740
TCTAACAAAG TCAAGATTCC CGGCTGGACT TTTGCAGCTT CCTTCCAAGT CTTCTGACC 1800
ACCTTGCACT ATTGGACTTT GGAAGGAGGT GCCTATAGAA AACGATTTG AACATACTTC 1860
ATCGCAGTGG ACTGTGTCCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA 1920
GATATGATAG GCCCGGAAGT TGCTGTGCC CATCAGCAGC TTGACGCGTG GTCACAGGAC 1980
GATTTCACTG ACACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG 2040
TTTAAACCAA ACGGAACCTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT 2100
GTATTAAC TG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC 2160
AGAATGGGGGA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA 2220

CTCATCCTTT TTAAATGAGA CTTGTTTCC CCTCTCTTG AGTCAAGTCA AATATGAGA	2280
TGCCTTGCG AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATT	2340
CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTAA CCTCAGGTT	2400
CAAATTCAAGT AAATTTGGA AACAGTACAG CTATTCTCA TCAATTCTCT ATCATGTTGA	2460
AGTCAAATT GGATTTCCA CCAAATTCTG AATTTGAGA CATACTTGTA CGCTCACTTG	2520
CCCCAGATGC CTCCTCTGTC CTCATTCTC TCTCCCACAC AAGCAGTCTT TTTCTACAGC	2580
CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCACCTT ATTCTAGGGT CTTACTCTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAA AAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met	
1 5 10 15	
Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn	
20 25 30	
Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu	
35 40 45	
Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu	
50 55 60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys	
65 70 75 80	
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val	
85 90 95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln	
100 105 110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg	
115 120 125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val	
130 135 140	
Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys	
145 150 155 160	

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
180 185 190

Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Leu Gly Val Val
195 200 205

Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
305 310 315 320

Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
355 360 365

Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
420 425 430

Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1929 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCANACANC GGCAGCTGAG GCGGAAACCT AGGCTGCGAG CCGGCCGCC GGGCGCGGAG	60
AGAGAAGGAA CCAACACAAG ACAGCAGCCC TTCGAGGTCT TTAGGCAGCT TGGAGGAGAA	120
CACATGAGAG AAAGAATCCC AAGAGGTTT GTTTCTTG AGAAGGTATT TCTGTCCAGC	180
TGCTCCAATG ACAGAGATAAC CTGCACCTT GTCTACTTC CAGAATGCC AGATGTCTGA	240
GGACAGCCAC TCCAGCAGCG CCATCCGGAG CCAGAATGAC AGCCAAGAAC GGCAGCAGCA	300
GCATGACAGG CAGAGACTTG ACAACCTGA GCCAATATCT AATGGGCGGC CCCAGAGTAA	360
CTCAAGACAG GTGGTGGAAC AAGATGAGGA GGAAGACGAA GAGCTGACAT TGAAATATGG	420
AGCCAAGCAT GTCATCATGC TCTTGTCCC CGTGACCCCTC TGCAATGGTCG TCGTCGTGGC	480
CACCATCAAA TCAGTCAGCT TCTATACCCG GAAGGACGGT CAGCTAATCT ACACCCCAT	540
CACAGAAGAC ACTGAGACTG TAGGCCAAAG AGCCCTGCAC TCGATCCTGA ATGCGGCCAT	600
CATGATCAGT GTCATTGTCA TTATGACCAT CCTCCTGGTG GTCCTGTATA AATACAGGTG	660
CTACAAGGTC ATCCACGCCT GGCTTATTAT TTCATCTCTG TTGTTGCTGT TCTTTTTTC	720
GTCATTTAC TTAGGGGAAG TATTTAAGAC CTACAATGTC KCCGTGGACT ACGTTACAGT	780
AGCACTCCTA ATCTGGAATT GGGGTGTGGT CGGGATGATT GCCATCCACT GGAAAGGCC	840
CCTTCGACTG CAGCAGCGT ATCTCATTAT GATCAGTGCC CTCATGCC CGGTATTTAT	900
CAAGTACCTC CCCGAATGGA CCGCATGGCT CATCTGGCT GTGATTCAG TATATGATTT	960
GGTGGCTGTT TTATGTCCTA AAGGCCACT TCGTATGCTG GTTGAACAG CTCAGGAAAG	1020
AAATGAGACT CTCTTCCAG CTCTTATCTA TTCCCAACA ATGGTGTGGT TGGTGAATAT	1080
GGCTGAAGGA GACCCAGAAG CCCAAAGGAG GGTACCCAAG AACCCCAAGT ATAACACACA	1140
AAGAGCGGAG AGAGAGACAC AGGACAGTGG TTCTGGAAC GATGATGGTG GCTTCAGTGA	1200
GGAGTGGGAG GCCCAAAGAG ACAGTCACCT GGGGCCAT CGCTCCACTC CCGAGTCAAG	1260
AGCTGCTGTC CAGGAACCTT CTGGGAGCAT TCTAACGAGT GAAGACCCGG AGGAAAGAGG	1320
AGTAAAACCTT GGACTGGGAG ATTCATTCTT CTACAGTGTGTT CTGGTTGGTA AGGCCTCAGC	1380
AACCGCCAGT GGAGACTGGA ACACAACCAT AGCCTGCTTK GTAGCCATAC TGATGGCCT	1440
GTGCCTTANA TTACTCCTGC TCGCCATTAA CAAGAAAGGG TNGCCAGCCC NCCCCATCTC	1500
CATCACCTTC GGGTTCGTGT TCTNCTTCGC CACGGATTAC CTTGTGCAGC CCTTCATGGA	1560

CCAACTTGCA TTCCATCACT TTTATATCTA GCCTTCTGC AGTTAGAACCA TGGATGTTTC 1620
TTCTTGATT ATCAAAAACA CAAAAACAGA GAGCAAGCCC GAGGAGGAGA CTGGTGACTT 1680
TCCTGTGTCC TCAGCTAACCA AAGGCAGGAC TCCAGCTGGA CTTCTGCAGC TTCCTTCCGA 1740
GTCTCCCTAG CCACCCGCAC TACTGGACTG TGGAAAGGAAG CGTCTACAGA GGAACGGTTT 1800
CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA 1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GGMCCGTGGG CATGGAGATT 1920
TACCCGCAC 1929

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15
Ser Glu Asp Ser His Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
20 25 30
Gln Glu Arg Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
35 40 45
Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
50 55 60
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
130 135 140
Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
145 150 155 160
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
165 170 175
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Xaa
180 185 190

Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Trp Gly Val Val
195 200 205

Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
210 215 220

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
225 230 235 240

Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
245 250 255

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
260 265 270

Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
275 280 285

Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
290 295 300

Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
305 310 315 320

Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
325 330 335

Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
340 345 350

Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
355 360 365

Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
370 375 380

Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
385 390 395 400

Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Xaa Val Ala Ile Leu Ile
405 410 415

Gly Leu Cys Leu Xaa Leu Leu Leu Ala Ile Tyr Lys Lys Gly Xaa
420 425 430

Pro Ala Xaa Pro Ile Ser Ile Thr Phe Gly Phe Val Phe Xaa Phe Ala
435 440 445

Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
450 455 460

Phe Tyr Ile
465

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA CGAGGGAAAT GCTGTTGCT CGAAGACGTC TCAGGGCGCA GGTGCCTTGG	60
GCCGGGATTA GTAGCCGTCT GAACTGGAGT GGAGTAGGAG AAAGAGGAAG CGTCTTGGC	120
TGGGTCTGCT TGAGCAACTG GTGAAACTCC GCGCCTCACG CCCC GGTTGTGT GTCCTTGTCC	180
AGGGCGACCG AGCATTCTGG CGAAGTCCG CACSCCTCTT GTTCGAGGCG GAAGACGGGG	240
TCTGATSCCT TCTCCTTGGT CGGGMCTGTC TCGAGGCATG CATGTCCAGT GACTCTTGTG	300
TTTGCTGCTG CTTCCCTCTC AGATTCTTCT CACCGTTGTG GTCAGCTCTG CTTTAGGCAN	360
TATTAATCCA TAGTGGAGGC TGGGATGGGT GAGAGAATTG AGGTGACTTT TCCATAATTG	420
AGACCTAATC TGGGAGCCTG CAAGTGACAA CAGCCTTGC GGTCTTACA CAGCTTGGCC	480
TGGAGGAGAA CACATGAAAG AAAGAACCTC AAGAGGCTTT GTTTCTGTG AAACAGTATT	540
TCTATACAGT TGCTCCAATG ACAGAGTTAC CTGCACCGTT GTCCTACTTC CAGAATGCAC	600
AGATGTCTGA GGACAACAC CTGAGCAATA CTAATGACAA TAGAGAACCG CAGGAGCACA	660
ACGACAGACG GAGCCTTGGC CACCCCTGAGC CATTATCTAA TGGACGACCC CAGGGTAAC	720
CCCGGCAGGT GGTGGAGCAA GATGAGGAAG AAGATGAGGA GCTGACATTG AAATATGGCG	780
CCAAGCATGT GATCATGCTC TTTGTCCCTG TGACTCTCTG CATGGTGGTG GTCGTGGCTA	840
CCATTAAGTC AGTCAGCTTT TATAACCGGA AGGATGGGCA GCTAATCTAT ACCCCATTCA	900
CAGAAGATAAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT GCTGCCATCA	960
TGATCAGTGT CATTGTTGTC ATGACTATCC TCCTGGTGGT TCTGTATAAA TACAGGTGCT	1020
ATAAGGTCAT CCATGCCTGG CTTATTATAT CATCTCTATT GTTGCTGTTG TTTTTTCAT	1080
TCATTTACTT GGGGGAAAGTG TTTAAAACCT ATAACGTTGC TGTGGACTAC ATTACTGTTG	1140
CACTCCTGAT CTGGAATTG GGTGTGGTGG GAATGATTTC CATTCACTGG AAAGGTCCAC	1200
TTCGACTCCA GCAGGCATAT CTCATTATGA TTAGTGCCCT CATGGCCCTG GTGTTTATCA	1260
AGTACCTCCC TGAATGGACT GCGTGGCTCA TCTTGGCTGT GATTCAGTA TATGATTTAG	1320
TGGCTTTT GTGTCCGAAA GGTCCACTTC GTATGCTGGT TGAAACAGCT CAGGAGAGAA	1380
ATGAAACGCT TTTCCAGCT CTCATTTACT CCTCAACAAT GGTGTGGTTG GTGAATATGG	1440
CAGAAGGAGA CCCGGAAGCT CAAAGGAGAG TATCCAAAAA TTCCAAGTAT AATGCAGAAA	1500
GCACAGAAAG GGAGTCACAA GACACTGTG CAGAGAATGA TGATGGCGGG TTCAGTGAGG	1560
AATGGGAAGC CCAGAGGGAC AGTCATCTAG GGCCTCATCG CTCTACACCT GAGTCACGAG	1620
CTGCTGTCCA GGAACCTTCC AGCAGTATCC TCGCTGGTGA AGACCCAGAG GAAAGGGGAG	1680
TAAAACTTGG ATTGGGAGAT TTCATTTCT ACAGTGTCT GGTTGGTAAA GCCTCAGCAA	1740
CAGCCAGTGG AGACTGGAAC ACAACCATAG CCTGTTCGT AGCCATATTA ATTGGTTGT	1800
GCCTTACATT ATTACTCCTT GCCATTTCA AGAAAGCATT GCCAGCTCTT CCAATCTCCA	1860

TCACCTTG GCTTGTTC TACTTGCCA CAGATTATCT TGTACAGCCT TTTATGGACC	1920
AATTAGCATT CCATCAATTT TATATCTAGC ATATTTGCGG TTAGAATCCC ATGGATGTTT	1980
CTTCTTGAC TATAACCAAA TCTGGGAGG ACAAAAGGTGA TTTTCCTGTG TCCACATCTA	2040
ACAAAAGTCAA GATTCCCGGC TGGACTTTG CAGCTTCCTT CCAAGTCTTC CTGACCACCT	2100
TGCACATATTG GACTTTGGAA GGAGGTGCCT ATAGAAAACG ATTTGAACA TACTTCATCG	2160
CAGTGGACTG TGTCCCTCGGT GCAGAAAACA CCAGATTGA GGGACGAGGT CAAGGAGATA	2220
TGATAGGCCCG GGAAGTTGCT GTGCCCATC AGCAGCTTGA CGCGTGGTCA CAGGACGATT	2280
TCACTGACAC TGCAGACTCT CAGGACTACC GGTTACCAAG AGGTTAGGTG AAGTGGTTA	2340
AACCAAACGG AACTCTTCAT CTTAAACTAC ACGTTGAAAA TCAACCCAAT AATTCTGTAT	2400
TAACTGAATT CTGAACCTTT CAGGAGGTAC TGTGAGGAAG AGCAGGCACC AGCAGCAGAA	2460
TGGGGAAATGG AGAGGTGGGC AGGGGTTCCA GCTTCCCTTT GATTTTTGTC TGCAGACTCA	2520
TCCTTTTAA ATGAGACTTG TTTCCCTCTC TCTTGAGTC AAGTCAAATA TGTAGATGCC	2580
TTTGGCAATT CTTCTCTCA AGCACTGACA CTCATTACCG TCTGTGATTG CCATTCTTC	2640
CCAAGGCCAG TCTGAACCTG AGGTTGCTT ATCCTAAAAG TTTAACCTC AGGTTCCAAA	2700
TTCAGTAAAT TTTGGAAACA GTACAGCTAT TTCTCATCAA TTCTCTATCA TGTGAAGTC	2760
AAATTGGAT TTTCCACCAA ATTCTGAATT TGTAGACATA CTTGTACGCT CACTTGCCCC	2820
AGATGCCTCC TCTGTCCCTCA TTCTTCTCTC CCACACAAAGC AGTCTTTTC TACAGCCAGT	2880
AAGGCAGCTC TGTCGTGGTA GCAGATGGTC CCACATTATTC TAGGGTCTTA CTCTTGTAT	2940
GATGAAAAGA ATGTGTTATG AATCGGTGCT GTCAGCCCTG CTGTCAGACC TTCTTCCACA	3000
GCAAATGAGA TGTATGCCCA AAGCGGTAGA ATTAAAGAAG AGTAAAATGG CTGTTGAAGC	3060
AAAAAAAAAAA AAAAAAAAAA AAAAAAAA	3087

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTNTCCNA CCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGC AACCAAATG	120
AGACACTGGC TCCAAACACA AAAACAAAAA CAAAAAAAGA GTAAATTAAAT TTANAGGGAA	180
GNATTAAATA AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGGANA	240

TTAATATCTA ATGTTGGGA GCCATCACAT TATTCTAAAT AATGTTTGG TGGAAATTAT	300
TGTACATCTT TAAATCTG TGTAATTTT TTTCAGGAA GTGTTAAAA CCTATAACGT	360
TGCTGTGGAC TACATTACTG TTNCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT	420
TTCCATTACAC TGGAAAGGTC CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC	480
CCTCATGNCC CTGKTGTTA TCAAGTACCT CCCTGAATGG ACTGNGTGGC TCATCTGGC	540
TGTGATTCAGTAA AAACCCAAGA CTGATAATTT GTTTGTCACA GGAATGCC	600
ACTGGAGTGT TTTCTTCCT CATCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC	660
ATCCCATAAC TCTTCAGTAA ATCATTAAATT AGCTATAGTA ACTTTTCAT TTGAAGATTT	720
CGGCTGGGCA TGGTAGCTCA TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCAGGAG	780
ATCACCTAAC CCCAGAGTTC AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA	840
GAAAATACAA AAATTAGCCG GGCATGGTGG TGACACACTG TAGTTCCAGC TACTTAGGAG	900
GCTGAGGTGG GAGGATCGAT TGATCCCAGG AGGTCAAGNC TGCAG	945

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTGG ATATATCAGT	120
AATAGTGCTT TTTTTTTTT TTTTTTTTT TTTGGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTGGCTCA CTGAAAGCTC CACCNCCGG	240
GTTCAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCGCCACC	300
ACGCCTGGGA TAATTTGGG NTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCCACACA GNATAAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTT AACCAGCCAA ACTAAAATCA CAGAGGSCMA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTAATTY TTTCMAAGTA GTTTACTTA TTTTCAGATT CTATTCTTT	300
ACTAGAATTAA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTAAAC	420
CCCCCAGGGA AATATTCACT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTGCC	480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC	516

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGATCCCTCC CCTTTTTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTAC TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGNAACTAAG AGTACCTAAC CTCCTGAAA TTGMAGNCCA	300
GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA	360
CGCCYCTGAC ACAAGGATT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT CAGTATTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTA AACTGCATAC TTCTGTACA	660
TTGTTTTTC TTGCTTCAGG TTTTAAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG	720
GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCCCT	840

GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTA GTCAGTCAGC TTTTATAACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTTCTTACA GCATGTCATC ATCACCTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCAGGGG GTTATTACTT	1200
CATGTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTTATTACTGG	1260
ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCCGCCATTG NTCTTCTGCC TAGAATATTC TTTCCTTNC TNACTTKGGN GGATTAAATT	1380
CCTGTATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTCC TTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTG GGACAAGGGG GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GACTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCTT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCAACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTNCNAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCTGG AGACCATATG ACCCATAGAG CTTAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTCTG ACTTTGTTAA TAGAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTTC	360
ATCCAAGGAC TCAATCTCCT TCTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480
ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600

CTKKNTGGCT GGGAAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA	660
GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACCTCCA GTTGCAATTA CTCTGCAGAT	720
GAGAGGCACT AATTATAAGC CATATTACCT TTCTTCTGAC AACCACTTGT CAGCCCNCGT	780
GGTTTCTGTG GCAGAAATCTG GTTCYATAMC AAGTCCTAA TAANCTGTAS CCNAAAAAAT	840
TTGATGAGGT ATTATAATTA TTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC	900
TTCACATGTT AAGTCCTTCT TTCCATATGT TAGACATTTT CTTTGAAGCA ATTTTAGAGT	960
GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA	1020
CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTTGGAGGT GGTAATGTGG	1080
KTGGTGATCT YCATTAACAC TGANCTAGGG CTTTKGKGTT TGKTTTATTG TAGAATCTAT	1140
ACCCCATTCA NAGAAGATAC CGAGACTGTG GCCCAGAGAG CCCTGCACTC AATTCTGAAT	1200
GCTGCCATCA TGATCAGNGT CATTGTWGTC ATGACTANNC TCCTGGTGGT TCWGTATAAA	1260
TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTGN TTTCCACCCCT GTTCTTCTTA	1320
TGGTTGGGTA TTCTTGTAC AGTAACTTAA CTGATCTAGG AAAGAAAAAA TGTTTGTCT	1380
TCTAGAGATA AGTTAATTTT TAGTTTCTT CCTCCTCACT GTGGAACATT CAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCAGG AGTCACAAG CAGCTGGGC AACGTAGCAA GACCCTGCCT CTATTAAAGA	1560
AAACAAAAAA CAAATATTGG AAGTATTAA TATGCATGGA ATCTATATGT CATGAAAAAA	1620
TTAGTGTAAA ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTTC AATGCCTTT TAGGCCATTG TCTCAAMAAA TAAAGCAGA AAACAAAAAA	1740
AGTTGTAACT GAAAATAAA CATTCCATA TAATAGCACA ATCTAAGTGG GTTTTGNTT	1800
GTTCGTTGN TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTG TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAGGAGTGGGA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCG GGACATAGTG	60
GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSGG ATCACTTGNG	120
GGTCNGGAAT NTGAGANCAG CCTGGGCAAN ATGGCGAAAC CCTGTCTCTA CTAAAAATAG	180

CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA	240
GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCACTG	300
CACTCCAGTC TGGGCCACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC	360
TTTTAAGGG TTGTGGGACC TGTTAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT	420
GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTT TTACATTCA TTACTTGGGG	480
TAAGTTGTGA AATTGGGGT CTGTCTTCA GAATTAACCA CCTNNGTGCT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTAATTGT NTCCACATAT	600
AGGTCAACT TGTTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACTTAAGA CTACAGTTAA TTCTAAGCCT	720
TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAACTCTTGT GCNATCAGAA TGTTNTAAA	780
GAAAGGGTNT CAAGGAATNG TATAANACC AAAAATAATT GAT	823

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTCCCA TCTTCTCCAC AGAGTTGTG CCTTACATTA TTACTCCTTG CCATTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTGAGG CTTGTTTCT ACTTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTG CATCAATTAA ATATCTAGCA	180
TATTTGCGGT TAGAATCCCA TGGATGTTTC TTCTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCCCGGCTGG ACTTTGGAG	300
GTTCTTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTAAC CAAACGGAAC TCTTCATCTT AAACTACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTCAAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCAACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT	720
TCCCTTGAT TTTTG	736

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 893 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGATCCGCC	GCCTTGGCCT	CCCAAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCTCCTG	60
GCTGAGTCTG	CGATTCTTG	CCAGCTCTAC	CCAGTTGTGT	CATCTTAAGC	AAGTCACTGA	120
ACTTCTCTGG	ATTCCCTTCT	CCTNNWGTAA	AATAAGNATG	TTATCTGNCC	NNCCTGCCTT	180
GGGCATTGTG	ATAAGGATAA	GATGACATTA	TAGAATNTNG	CAAATTAAA	AGCGCTAGAC	240
AAATGATTTT	ATGAAAATAT	AAAGATTAGN	TTGAGTTGG	GCCAGCATAG	AAAAAGGAAT	300
GTTGAGAAC	TTCCNTTAAG	GATTACTCAA	GCYCCCCTT	TGSTGKNWAA	TCAGANNGTC	360
ATNNAMNTAT	CNTNTGTGGG	YTGAAAATGT	TTGGTTGTCT	CAGGCGGTTC	CTACTTATTG	420
CTAAAGAGTC	CTACCTTGAG	CTTATAGTAA	ATTTGTCAGT	TAGTTGAAAG	TCGTGACAAA	480
TTAACACATT	CCTGGTTTAC	AAATTGGTCT	TATAAGTATT	TGATTGGTNT	AAATGNATTT	540
ACTAGGATT	AACTAACAAAT	GGATGACCTG	GTGAAATCCT	ATTCAGACC	TAATCTGGGA	600
GCCTGCAAGT	GACAAACAGCC	TTTGCAGTCC	TTAGACAGCT	TGGCCTGGAG	GAGAACACAT	660
GAAAGAAAGG	TTTGTTCCTG	CTTAATGTAA	TCTATGGAAG	TGTTTTTAT	AACAGTATAA	720
TTGTAGTGCA	CAAAGTTCTG	TTTTCTTTC	CCTTTTCAGA	ACCTCAAGAG	GCTTGTGTT	780
CTGTGAAACA	GTATTCTAT	ACAGTNTGCT	CCAANTGNAC	AGAGTTACCT	GCACNNCGTT	840
GTCCNTACTT	CCAGAATGCA	CAGATGTCTG	AGGACAACCA	CCTGAGCAAT	ACT	893

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCAGAAAATA	CTTTNGGGCA	CATGAGAAC	ACATGAGAAC	AAGCTGATGC	ATAATTCC	60
CTGTGATGGA	ATGTAATAGT	AATTTAACAG	TGTCCTTCT	TTTTAAGTGC	CTCAAGGATA	120
CAGCAAATA	AAACAAAAGC	AATATGAAGG	CTGAGAAC	AGTACAGATT	ATCATAAAAA	180

GTATAGATCA AAAGGAATCT GGTKCTNAGG TTGGCGCAGC AGCCTCTAGA AGCGACNAGG	240
GAGACTTTA GAACTACCAT TCTCCTCTAT AAGTGGATCC NANGCCCAGG RAAACTTGAT	300
ATTGAGNACA ATGGCCTTAC TGAAATAACC TGTGATCCAC TCGGNCTCAT CATCTCCACC	360
ACCACCATAA ATTTGATGAG TNCCTATAAT ATTCCANCCA GNNGAAATAC CTGGRAGGTT	420
ACTGAAAGGC NACNATCAGA CNAAAATAAA GNATACCGTA GGTAAATTCT ACAGT	475

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTCCTCNAGA TCTCTTCAAA ATTCAATTNTG CGCTATAGGA GCTGGGATTA CCGCGGGTGC	60
TGGAACCAGA CTTGCNCTCC AATGGATCCT CCANACNGGA NGGGGGGTGG ACTCACACCA	120
TTTACAGGGG GCTCGTAAAG AATCCTGTT TGANTATTNT NCCGTCAATT ACCNCCCCAA	180

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AATGTAACMA CMAAACCYCA AACTCCTGNA AGAANATGGT TACTTATNGA TNCCATTN	60
TTTTNCACT CTCAGACATA AATATAAACM MANTTCTAC TGTGGRAAAA CATCTNCAGG	120
GGNCNTTAN CCATGATCTC TAGNACNANG GGCTNGTGGN TNGTTTAAT GTCTCTAAGC	180
NACTNGACTA GTTTCTCTN CACTGAGNAA ACTGCNACAA GTNNNTNCTN CTGNATCTGN	240
ACTGNAATGC TAAGTTNCAA GTNCCAATGA GCTNGTGANT TANYCTTTAT TTNAMCNAAA	300
GTNNNTTAATC ANCCNCAGTG TTACTTTGNA AAGCTNCTCC CTGGACAGGC GGCCCNACTT	360
CTAATGTTAT GAATGGGCTG GAGNANCCTC NACNTGAGTT TNNWAAGGNT CAACANCCAA	420
TRGNAANTGT AMCCGACTCT AAATTCCAAC CNATAAT	457

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCTGTGCTA GGTAGTGTAC TAATCATTCA GTTTATCTCA TTTAATCTNN ATGNAACTCT	60
AAGTCATTG CTNTGANCNA CACATAACAG ATCTCGAAC TGNAGTTAG CGAGGCCAGT	120
TAATTTKCCA AAGNTCATAA TNCTAAGNAG TTCTAGNATG GAGATTCTMAA GTCCNACTGT	180
TTAGTCAAGA GACCCTACTG TTAACTAGTA CCTTTACACT ACTAACTGGG TAANCCATAA	240
NCAATTAATG ATAAAGATTG AGATTACTKC CACATTCTCA CTGGTTATAA ATTAAAACNT	300
CAAATAAAAA NTCTTGGCAC TTCTATGGTA ATATTTTAT TAGGATAAAC TTTCAAGNAG	360
TGGATNCTAG GTG	373

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCACACTGN TGGGCCATGG AAGCCATGAG TGTACCACAT GGCCCTGTCC CACTGGCCAC	60
AGTNGATTGG TTGGNTCGGG AGTAGTCACC TGATTCAAGN TGGGCCAATC AGATCCTACC	120
TCCANGGGGT TNAGGAATTAG AAAACAGTGA CCCTAGYTAG TNTAGGCNAC TTGAACTGGA	180
GGGCCCATAC ATTCAAGGAGC CTTATGGGC CATGTACACA TGGAAGCAGG AAGANTGAAG	240
GAGGGAGAAG TAGAGGCCAG AAACCCACCT GGGTCCCTGT TTCCCAATGN TAAGTCCCTG	300
CCATGTYCCT GCTCTCCTG TGGTTNGGAT CTTCAAAGGT TGCTCAAATT NGGGGCAGTG	360
GCCCTGGCAG CTTTCAAAT CCTYCCCATT TTTATTGAAG CTGAAAGACC CTTGACTAGA	420
AC	422

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATTGTTATTT	TTCGTCACTA	CCTCCCCGGG	TCGGGAGTGG	GTAATTTGCG	CGCCTGCTGC	60
CTTCCTTGG	GTGTTAGCC	GTTTCTCAGG	CTCCCTCTCC	GGAATCGAAC	CCTGATTCCC	120
CGTCACCCGT	GGTCACCATG	GTTAGGCACG	GCGACTACCA	TCGAAAGTTA	ATAGGGCAGA	180
TCTCGAGAAT	TCTCGAGATC	TCCNTCMAAT	TATTACTTCA	NTTKCGGTAG	TGATCAGNAC	240
NAGGCAGTTC	TATTGATTTC	TCTCCTTCA	TTCTGAGTTT	CTCCATAAAAT	TAATTGGACC	300
TAATCATGTT	TKNAATCCTG	TCTTTAGGG	GGNANTTGNA	CTNTCAAGTG	TTTAAAGGGA	360
GGGNCGGAGN	ATGATTNTGG	ATTGGAGTGA	GAGCA			395

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CAGANTTCT	GGGTNAAAAG	GACCTNANAC	ATAATATAGT	GGACTTNCAA	TAAACACTTA	60
CCAAATGGAN	AAATGAACCC	CTGGTCACCC	CGATCTCACT	AGTNCCNCC	CTGAAACCCG	120
ANANATCTGA	GTCCTTTCT	CCTTTACTAA	CCCTTNCTCC	AATCCTGCTC	ATGGGAATTA	180
ANGNTGTAAA	ATANGCCTGG	GGNACCTCGG	RCCTCTNCCC	TGGGNTCTGT	GGGTGGGAGN	240
ACTGTGGAAG	CCGTWTCAAT	CGCCCCCACC	TATGAGAGCC	TTTCTNCAGG	GCCAGCCATG	300
AACGTCCCCC	ATGTNATCAG	NATTCAGG	CTACTGCTGT	CCTTCYTGGA	TWTTAACCT	360
GGRGCGGGC	CAGGGACAGA	AAARGGAGGT	GGCAAGATCC	TTGAACAAAA	GGAGCTATAAA	420
AAGGGCGTTG	GGGAAAGCAA	GGCAAACGGC	AGATTAACAA	AGCAGGCACC	TCAAGGAAAC	480
GTGACGC						487

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCGAGATCT	GGCCCACATCAT	TTAGTTTAT	NGCTTGAGT	NTNTAGNAGA	TAAAACATCC	60
ACGTGGATCT	NCTCTTAGAG	AAATCAANTA	CTTTAGGNAT	NTGATAGTCA	GAGANTGGNT	120
ATCAAATNGA	AAGGNATNTN	GGTNGANCAG	TTAGTTNGYN	CCNTTNGNNG	AGACCACTGG	180

GNTGTNGASA CCAGATTCKM GGGTNCNAAT CTTANGTAA TCTNAGAGCC AACACATGGG	240
TCATNTTATS CCCCCAAACTT AGCCACATCT BGTGGGYTA TGGNGTCACC CCAAGAGCAG	300
GAGGAGCATG GNTGGATGGA AATCCATCTC CACCACTGGA ACCCCAAWTT CTGAATGNAT	360
CACCTGTTAG AGTTTCTTGT YCATAAAAATA GCAGGAAATT TAGGAATTAA GTTTTTTTT	420
AATAGTTGG GCCTTTATC CACACTCTCA GGAGCTTAGG ATACTTTCT CCTTCAGCTC	480
ACTCTGAAAC TCCCTCTGGA	500

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCGAGATCTG TGGTAGTNAC ATGATATTCT GGCAMCTACT TTCATTATCA CCTTTATTAA	60
AATAAATTAA AAGAAAAATG GCAGTATGTT TCTGTGRAGN CCACGAGTAC TCATTTAAA	120
GGACTCMAGA GTTNCAGRNA AGTAAAAGR AAAGAGTAAA ATCATTCTT AANTYTYWYY	180
TTCCAGAAAT AACGATGTTG AGCATTAAAGT GGACTTCATT TCATACTCTT TCMMAGNTTA	240
TGTAGGCATA WAWATGTGTG TGTATATACA TATATATGGG TACATCCTTA GAGAAGTTGG	300
CTGGCTAGAT AGACACACNT NAAAAATGGR ATCATACTCT AATKCCATT NNANTTTANA	360
AAATACATAT TCAGANCCNC TGTNCTTATA NACAGAGTAA NTGAAA	406

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GACCCAGTAA AACTTATCTC ATGAGCATAA GGCTGAATGG GATTGACAGC CTACAGAAC	60
CGGATTTAT CATGAGGGCA TTAGTGGGG TTGGGGGTTA GGTACTGAAA GTTTAAGGAG	120
GTGAAAGGAA AGCAACTTGT GCCTTACAGG GTCAAGCTAG GTCAAGGAAA TTCCCAGGAG	180
CGTGTGGAAG CTCTCTACCT GATAGGTGAG CTCAAGCTTA TGACCGCCCA AGCTTCTCCC	240
CAAGCTTCCC TTCCACTGCT TCCTCTTGAT TGACTTCCAC AGCAAGGTC	289

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATCAGGAT TTACTGAGTA AAAATCTAG	GTNTTAACCA TGCCCCTAAA ATGTGCTATN	60
CCAAAGAGGA ACAGGTTACT TGGGAGGAAA AAAGCTGCCT	GGGNAACTCC CCNCAAATGT	120
TTATTTAAA TAAAATGGT NGATGGAAT ATTTNTAAA	AGAACTTGGG GTNTAATATG	180
GNATACTGCC CATCAAACAA AAAAGGAAAT AAAACTTCNT	TCCCATTTAT AATAAGTTNC	240
CCACCCTTA CTATCAAGAT TACAACTTAT	TGACCTTTA TGCTNGCTNG	300
GAECTGCCTAA TCCAATGTTT AAATTTCTA NGTCTGNATT	TCAATGTGGG TAGGAGTNAT	360
TTTCAAA		367

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGTATCTGA CAGGTAAGAT TGCTTTTAA AGTTGTTTA AATGCATTAC ATGACTGAGA	60
AAAGAAAAAT GCACATTTA TTGTTGCAGT TTAAAATTTC ATTTNGNGTG AACTAAACG	120
TGAAACAAAA GGGATAAAATG TGTTTGNTT TTGTTTGTT TTTACCTGTT TGGGTATTT	180
TTTTCTGAGT TTGTGTAGAA ACCCGTGTGG NTACACTGGG TAATCTTGTCA AGGGNTACMA	240
AMCTTGGTC TTGANTTTGG TTANTTGGNT TTANTTGGTG NACCCATGTA CTTGCTCTTC	300
CNTCCCAGAA ACATAGCTTG GTAGGCNAGG GTTAANCCAG TGTCGGCGAN CCCATGTCCC	360
TANCACAGCA TCTTGTAAAGT TTAATGCACA ATCGTTCCNT CCCAGGATGG ANTATCATT	420
ATAAA	425

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2377 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAGAGGCAGCA CGAGCCACAA ATAAAGCAAG AGCCAGAAC AGAAGNGGAG GAAGAAGAAA 60
AGCAAGAAAA AGRAGRAANA CGAGAAGAAC CCATGGRAGA GGAAGAGGAN CCAGANCMMA 120
AGCCTTGCTC GAAACCTACT CTGAGGCCCA TCAGCTCTGC TCCATCTGTT TCCTCTGCCA 180
GTGGNAATGC NACACCTAAC ACTCCTGGGG ATGAGTCTCC CTGTGGTATT ATTATTCCTC 240
ATGRAAACTC ACCAGATCAA CAGCAACCTG AGGAGCATAG GCCMAAAATA GGACTAAGTC 300
TTAAACTGGG TGCTTCAAT AGTCCTGGTC AGCCTAATTG TGTGAAGAGA AAGAAACTAC 360
CTGTAGATAG TGTCTTTAAC AAATTTGAGG ATGAAGACAG TGATGACGTA CCCCCAAAAA 420
GGAAACTGGT TCCCTGGAT TATGGTGAAG ATGATAAAAA TNCAACCAA GGCAGTGAA 480
ACACTGAAGA AAAGCGTAAA CACATTAAGA GTCTCATTGA GAAAATCCCT ACAGCCAAAC 540
CTGAGCTCTT CGCTTATCCC CTGGATTGGT CTATTGTGGA TTCTATACTG ATGGAACGTC 600
GAATTAGACC ATGGATTAAT AAGAAAATCA TAGAATATAT AGGTGAAGAA GAAGCTACAT 660
TAGTTGATTT NGTTTGTCT AAGGTTATGG CTCATAGTNC ACCCCAGAGC ATTTTAGATG 720
ATGTTGCCAT GGTACTTGAT GAAGAAGCAG AAGTTTTAT AGTCAAAATG TGGAGATTAT 780
TGATATATGA AACAGAAGCC AAGAAAATTG GTCTTGAA GTAAAACATT TTATATTTAG 840
AGTTCCATTT CAGATTCTT CTTTGCCACC CTTTAAGGA CTTKGAATTT TTCTTGTCT 900
TKGAAGACAT TGTGAGATCT GTAATTTTT TTTTTGTAG AAAATGTGAA TTTTTGGTC 960
CTCTAATTTG TTGTTGCCCT GTGTACTCCC TTGGTTGTAA AGTCATCTGA ATCCTTGGTT 1020
CTCTTATAC TCACCAGGTA CAAATTACTG GTATGTTTA TAAGCCGCAG CTACTGTACA 1080
CAGCCTATCT GATATAATCT TGTTCTGCTG ATTTGTTCT TGTAAATATT AAAACGACTC 1140
CCCAATTATT TTGCAGAATT GCACTTAATA TTGAAATGTA CTGTATAGGA ACCAACATGA 1200
ACAATTTAA TTGAAAACAC CAGTCATCAA CTATTACAC CCCCACCTCTC TTTTCATCAG 1260
AAATGGCAAG CCCTTGTGAA GGCATGGAGT TTAAAATTGG AATGCAAAAA TTAGCAGACA 1320
ATCCATTCCCT ACTGTATTTG TGATGAAATG TGTTGTGAA TGTATGTGTA AAAGTCTTC 1380
TTTCCCTAA TTTGCTTTGG TGGGGTCCTT AAAACATTTC CCAACTAAAG AATAGAATTG 1440
TAAAGGAAAA GTGGTACTGT TCCAACCTGA AATGTCTGTT ATAATTAGGT TATTAGTTTC 1500
CCAGAGCATG GTGTTCTCGT GTCGTGAGCA ATGTGGTTG CTAACGTAT GGGGTTTCT 1560
TATTAATAAG ATGGCTGCTT CAGCTCTCT TTTAAAGGAA TGTGGATCAT AGTGTATTTT 1620
CCTTTAATT TTATTGCTCA GAAATGAGGC ATATCCCTAA AAATCTCGGA GAGCTGTATT 1680
TAATGCATT TTGCACTAAT TGGTCCTTAG TTTAATTCTA TTGTATCTGT TTATTTAAC 1740
AAAAATTCAT CATATCAAAA AGTGTAAAGTG AAAACCCCT TTAAACAAA ACAAAAAAAT 1800
GAAATAAAAT TAGGCAAATT GACAGACAGT GAGAGTTTA CAAACATGAT AGGTATTCTG 1860
CTCGGCAATT TGTAAGTTA CATGTTATT AAGGATAAAAG GTAAATCATT CAAGGCAGTT 1920

ACCAACCAC T AACTATTGT T TTCATTTT GTCTTGTAGA AGGTTATAT CTTGTTTAC	1980
CTTGGCTCAT TAGTGTAA AAATGTACTG ATGATGTGCT TAGAGAAATT CCTGGGGCTT	2040
TCTTCGTTGT AGATCAGAAT TTCACCAGGG AGTAAAATT CCTGAAAACG TAAGAAGTTT	2100
TAAACAGCTT TCCACACAAA TTAGATGCAA CTGTTCCCCT GTCTGAGGTA CTTATTTAAA	2160
AGAAAAGTAA AGATTGGCCT GTTAGAAAAA GCATAATGTG AGCTTGGAT TACTGGATTT	2220
TTTTTTTTT TAAACACACC TGGAGAGGAC ATTTGAAAC ACTGTTCTTA CCCTCGAACCC	2280
CTGATGTGGT TCCATTATGT AAATATTTCA AATATTAAGA ATGTATATAT TTGAAAAAAA	2340
AAAAAAAAAAA AAAATCCCTG CGGCCCGCAAG GGAATTC	2377

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATTGGAGCTC CACCGCGGTG GCGGCCGCTC TAGNAACTAG TGGATCCCCC GGGCTGCAGG	60
AATTCTCGAG ATCTCCCCCA AGTAAATGAA TGAAAAAAAG AACAGCAACA ATAGAGATGA	120
TATAATAAGC CAGGCATGGA TGACCTTATA GCACCCGTGA TTTATACAGA ACCACCAGGA	180
GGATAGTCAT GACAACNATG ACACTGATCA TGATNCCAGC ATTCAAGATT GAGTNCAGGG	240
CTCTCTGGCC CACAGTCTCG GTATCTTCTG TGNATGGGT ATAGATTARC TGTCCATCCT	300
TCCGGGNATA AAANCTGACT GACTTAATGG TANCCACGAC CACCACCCAT KCAGAGAGTC	360
ACAGGGACMA AAGAGCATGA TCAACATGCT TGGCNCCATA TTTCAATNTC ANCTCCTCAT	420
CTTCTTCCTC ATCTTNCTCC ACCACCTNCC GGGAGTTAAC CCTGGGGTCG TCCATTAGAT	480
AATGGCTCA	489

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGGTGCTTC AGTGTGGCTG ACACAGCAGC ATGGTCTTGA CAAGTTTCT TCATCCTACC 60
ACAAAATCCC AGTTGGTAAT AGAGACTTTA CTCCTACCTA TCAAAACAC AAAATGTCCC 120
ATTAGGGGGG GACATGTTGT ACATGTTAGG ATCATTCAAA TAACCAAGAT TATAAGGTGA 180

GGAAAGATGC CCCTAACTGA TTCTTTGTC TCTCATCTTGTGGGGTCAATCT TCTGGTSSTG CCTCTCCAGG TCTCTCCAG GCCGGTCATA GACGTACTCCCTCTGAGGCC GACCGATGGTTAGAAGAGGT GTCTAAGAGC GTCCGGGCTC AGCAGCCCCAGCCTCAGCT GCTCCTCTGC AGCCAGTTCT CCAGCCTCCT CCACCCACTG CCATCTCCAGCCAGCATCA CCTTTCCAAG GGAATGCATT CCTCACCTCT CAGCCTGTGC CAGTGGGTGTGGTCCCAGCC CTGCAACCAAG CCTTTGTCCC TGCCCAGTCC TATCCTGTGG CCAATGGAATGCCCTATCCA GCCCCTAATG TGCCTGTGGT GGGCATCACT CCCTCCCAGA TGGTGGCCAACTGCTTGGC ACTGCAGGCC ACCCTCAGGC TGCCCATCCC CATCAGTCAC CCAGCCTGGTCAGGCAGCAG ACATTCCTC ACTACGAGGC AAGCAGTGC ACCACCAGTC CCTTCTTTAACCTCCTGCT CAGCACCTCA ACGGTTCTGC AGCTTCAAT GGTGTAGATG ATGGCAGGTTGGCCTCAGCA GACAGGCATA CAGAGGTTCC TACAGGCACC TGCCCAGTGG ATCCTTTGAAGCCCAGTGG GCTGCATTAG AAAATAAGTC CAAGCAGCGT ACTAATCCCT CCCCTACCAAACCTTCTCC AGTGACTTAC AGAAGACGTT TGAAATTGAA CTTAAGCAA TCATTATGGCTATGTATCTT GTCCATACCA GACAGGGAGC AGGGGGTAGC GGTCAAAGGA GCMAAACAGAYTTGTCTCC TGATTAGTAC TCTTTCACT AATCCAAAG GTCCAAGGA ACAAGTCCAGGCCAGAGTA CTGTGAGGGTGATTTGAA AGACATGGAA AAAAGCATTCTAGAGAAAACTGCCTTGC AATTAGGCTA AAGAAGTCAA GGAAATGTTG CTTCTGTAC TCCCTCTCCCTTACCCCT TACAAATCTC TGGCAACAGA GAGGCAAAGT ATCTGAACAA GAATCTATATTCCAAGCACA TTTACTGAAA TGAAAACAC AACAGGAAGC AAAGCAATGT CCCTTGTGTTTTCAGGCCAT TCACCTGCCT CCTGTCAGTA GTGGCCTGTA TTAGAGATCA AGAAGAGTGGTTTGCTCA GGCTGGAAC AGAGAGGCAC GCTATGCTGC CAGAATTCCC AGGAGGGCATATCAGCAACT GCCCAGCAGA GCTATATTGTTT GGGGAGAAG TTGAGCTTCC ATTTGAGTAACAGAATAAA TATTATATAT ATCAAAAGCC AAAATCTTA TTTTATGCA TTTAGAATATTTAAATAGT TCTCAGATAT TAAGAAGTTG TATGAGTTGT AAGTAATCTT GCCAAAGGTAAGGGGCTAG TTGTAAGAAA TTGTACATRA GATTGATTATCATTGATGC CTACTGAAATAAAAGAGGA AAGGCTGGAA GCATGCAGAC AGGATCCCTA GCTTGTGTTCTGTCAGTCATTCATTGTAAG TAGCACATTG CAACAACAAT CATGCTTATG ACCAATACAG TCACTAGGTTGTAGTTTTT TTAAATAAAG GAAAGCAGT ATTGCTCTGG TTTAACCT ATGATGGAATTCTAATGTCA TTATTTAAT GGAATCAATC GAAATATGCT CTATAGAGAA TATATCTTTATATATTGCT GCAGTTCCCT TATGTTAAC TCTTAACACT AAGGTAACAT GACATAATCATCCATAGAA GGGAACACAG GTTACCATAT TGTTTGTA TATGGGTCTT GGTGGGTTTTGTTTATCCT TTAAATTTG TTCCCATGAG TTTGTGGGG ATGGGGATTC TGGTTTTATT	240 300 360 420 480 540 600 660 720 780 840 900 960 1020 1080 1140 1200 1260 1320 1380 1440 1500 1560 1620 1680 1740 1800 1860 1920 1980 2040 2100
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AGCTTTGTGT GTGTCCTCTT CCCCCAAACC CCCTTTGGT GAGAACATCC CCTTGACAGT	2160
TGCAGCCTCT TGACCTCGGA TAACAATAAG AGAGCTCATC TCATTTTAC TTTTGAACGT	2220
TGGCGCTTAC AATCAAATGT AAGTTATATA TATTTGTACT GATGAAAATT TATAATCTGC	2280
TTAACAAAA ATAAATGTTC ATGGTAG	2307

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCAGCTATT TACATGGCCT CACAGGCATC AGCTGAAAAG AGGACCCMAA AAGAAATTGG	60
AGATATTGCT GGTGTTGCTG ATGTTACAAT CAGRCAGTTC TATAGACTGA TCTATCCTCG	120
AGCCCCAGAT CTGTTCTTA CAGACTTCMA ATTKGACACC CCAGTGGACA AACTACCACA	180
GCTATAAATT GAGGCAGYTA ACGTCMAATT CTTGANNACM AAACCTKNCC TGTTGTACAT	240
AGCCTATACM AAATGCTGGG TTGAGCCTTT CATAAGNAA AACMNAAGAC ATGGNTACGC	300
ATTCCAGGGC TKGANTACTT ATTGCTTGGC ATTCTTGTAT GTA	343

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAGGGCTAA CCAGCCACTG CACCAAAATT AGTCCTTACA TTATAATACT CTGGCCATTG	60
GAAGAGAAAA ATGGGAAAAT TCAACAATT GAAAGACTAT GATCCCTCTG GCTCATGATC	120
TACTGACCAAG AATGAAAGTCC TGAAGGATT CTTCTGTTA TGTTATCTAC CCAGCTAATC	180
TCAAACAAGA GGAGCTGGAA AGAACAAAGC CCCATGAAGC TACCCCTAGA CCCAGAAAGC	240
CAAGAACAGG GCCAAGAAAA TGAACAGCAG ACAAGCCTGA AATAGAAGTG GNACAGACAT	300
GTGGNAAGAC CAAGTACACC CAGTTNGGTG GTAAAGATTC CGATATCAAG CTTATCGATA	360
CCG	363

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 362 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTACATGGT TTCTTGNC	CCCCASCCAC CTTCCCAT	CTCTACCGGY TGATAGTCTC	60
TCAGNTAGTA GACCTTTCT	NGTTTAGRCA GGGCACNTT	TTTAAAAACT CCAGACGGGT	120
ACCCCTCCATG TKGMAGGC	GA CGTGGCCCTG GATCACTCAA	CTGANTGTCA TNKGANTGGT	180
GCCCCCAGAG TGAGGACAAT	GGTGNAGCCC TCCTAAGGCC	CTNCCTGAGT GTCCCTCCTT	240
CATGAAGATG ATTCTGAGGN	TTCCCAGGCC TNCACCCTTC	TTKGAAARCC CATAGNAGTT	300
CATATGNACT NCTCTNCTAT	GCTCACCAAA CTCTNCCTTC	ATCATACTTG GGGGATGTGT	360
GT			362

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 475 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GTGCATGTAA TTACAGTTAC	GATATATGAA ACGTACAAA	TATTATGAGT ATATAATATG	60
GGGAGACTTA ATCTAGTTG	GGGGATCAGG GCACATTCT	CTAAGAAAGT GACATTGAA	120
TTGAGCTCTG AAGGATAAAAT	AGACATTACC CAGAAGAATA	AAATGATGGG GAAGAAGGAG	180
GACATTTCC GTAGATTCC	AGTGGCCCCN CTTGATCCCT	TATCCACTCA TCACTNAGGA	240
GGATATTAAA TKCTATAGAA	ATGGRAGRAA GACMMAAAGA	GACCCTNATA TCTCGAGAGG	300
ATCCAGCMAA ATTCCAAGAG	ACACAACAWT AAGAAACTNG	GAAGGAAGAG AAAAGGCMMN	360
NNAGGNAAAA GAAAGACAAG	GAAATTNWNN NAGNACGGAG	AGAAAGAGAG AGGGAGCGTN	420
NAAGGGNACG AGAAAGGCGA	GNACGGGAC GAGAAAGGGN	AAGAGNACGT AAACG	475

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 346 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGAAATAAAT GAGATCTCAG TGGTGGTATG GATTGGACTG ATCTCTGTAA CTGTGTNTGG	60
AAAAAGGACC GGAAAATGAA AGCCAGATCC CAGTAAGGGG TAGAGAGGGG CCAAGAGAAC	120
TGAACATCTG GGCTGCCGGA GAAATCAAAG TCTAGGAAGT AAGAGGTAAG AGTGTACTAC	180
AGGGGACATA CCCCAATCTC TTGGTCCCT CCCTCTNCCT TCCTCTCCCA GAGACCCAGG	240
TCCCTGGGAC TATNTTGGAT CTGTCTCTGA AGCTGAAAAA CAAAAGGCAG AGGAGACAGT	300
CGGNTCTAAG TGACCAATCT CAAGCCAGCT TGGTCAGAAN TCCTAA	346

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 433 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAATCCAGTG CAGGCAACAT TATGTGGAAA TAGAACAGG GCTCCTGCTA GGAGATTGAN	60
ATTCTGGCTT TCCTTGGAA CCCCTCACTG ACTCATGCC CCTGAANCAG GANCCANCAG	120
GTNCCAAGGC TCCCCTGCTC CTNTCCCTNC CCCAGGGCGA GATAGGAARC CGGAARCTG	180
GGCAGGCTGA RCCCANCCGA CTGGAACCAAG GGNAGANCCT GTGGGTGGGT GGNAGGGAGG	240
GAAGGAGGCC AGATTCTCC AGAACTGGGG RAGAGAACAG GTTTTGGAAAG TTGGGGGAGG	300
GTTCGGGTTT CACAGTGATG GTTTCATGAN ACCCTGGAGG GTTNCACACT CCTGGTKCAN	360
TTTTGNTANT CGTNCTTGAA ANACARNCCG CTTCCCTTCA ACCCTCCNCN TAAAAAGTTT	420
TGATNTTTTA AGG	433

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ACCAAGAGCC CCCAGTTAT GNTAACTCTC ATGACAAACA CAATTTAGT ACCTCTCACT	60
ACCAACTATC CAGGAACCAAG GANTCACCTA TTACTACGGT TCCAGCAGAA TGGGAATCCC	120
ATTCTCGGAT ATCCAGGGTA AATCCCTGAC CATGTGAGAG GAATCCTAGT GCCCCAACAA	180
CCTCACCCCC TGACTCCTCC TCAANGCTC TGCCAAGTCA ACAAAAAAAAT CCTCTACATT	240

TACACTATCT GTAAAGCCAA AGACCAGCGT CAACCTAAAT GTCCATCAAT AAGGGAATGG	300
TTGGATAAGT AAAAATTATG CAGCTGTAGG AAGGAATGAA GAATGTCTAT	350

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 512 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAAGGGAACA AAAGCTGGTA CCGGGCCCCC CCTCGAGGTC GACGGTATCG ATAAGCTGGA	60
TATCGAATCC TCGAGATCTA CCTAAAAAAA AAAAATTAAC TTCCCAAATG TGGGAGTCTA	120
CTCTGTTCCC TCCTNGTNTT TATTNCTGTN TACTTTYCTA ANATGGTTAA AATGTGTAAN	180
CAATATGTGT CCTTTNACTN KGGKGTGAAC ATTTTTYCTA TTATAAATYC TWAGAAAATA	240
TTNCTATGGN TATGAGATAT TKGATTCCAA GTGCCTKGTA ATTTACTYCT CAAATGTCCC	300
TGATGTTKGGA NATTKGTTNC TAGTGTTCAGT CTATTAAAA AAACAGNAAT ATCTGTCTNT	360
ATGCTNAGAG CTTNTYCAAGT TTYCAAATTA TTNCCTTAGG GTAAAATCCT AGAAGTAGAA	420
TTTTGGGGC AAATTATCTA CATATTATA ATTGTCTGG TATTCCAAAT CTCGTTTCC	480
AAAAGCTTAT ATCAATTGT ACTTAACACC AG	512

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATTTAAGATG ACTGGGGGTC TCTNCCTAAT CCCATACTCC ACTGGAGAGG ANAAGTGGGA	60
AAGGTTGGTC TAGTTARGGT NGNTGGGGAC CCTCCCAAGA GCTGNAGAAG CAGAGATAAG	120
NAGAGCCTNC TNCTAAATCC ACATGGNCCT YCCAAGGNTC TCATCCTCTA GGACCTACCA	180
CTNCTCAGTC TACTTACTTG TCTYCTGANA TGCTTCTNG AGGGGNAGAA AACAAAGGAA	240
GAGTAATAAC AAGCAGNAGA AACTGCAGAG AATGAAAAT AAGTCCATAG GAGAATGTTG	300
NAAATAGAAT CATCCNCCTT TACATATTGT CACTCCAGGA AAACTGCCAA GAACCACTCA	360
TTCCCTCTAGA TACAMTCCT GTAGGATCCY CCCAGACTTC CTCCCTTAAG CACGTCAGTA	420
TTCTCCTTAT TCTCCCTTCA TTTCAACCCT	450

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGATCTGC CCCAGCCCAC ATTCCTTTG TTGAATGAGT AGAGAAGACT GAGAAGTATC	60
ACTCACCGT GATGTGGTTT GTCCCTTTTC CAGCCAGTGT GTTGGTAATA AAAGTCACCT	120
TTCAGAGCTT TGGTCCCCGT AATGCCCGTC TTTCCTGTGT CCAGGAATAA CCTTGNTAC	180
TAGGCAGTCC TCTGAAAGAT TTGTAGAAGG TTAAAGTGGA AAGGGACTTG GAAGCTCATA	240
GAATCCATGC CTCTTCTTT AGCATCAAGG AATTAGAAGT CCTGAGAGAT GAAGAATGTT	300
GTCTTCCCAA CTCAAACCCA TTTCTTGAAG CCATTCCCT GTTACTGNA TTGCCACAA	360
CCCTTCCCCC TTGNTATCCT CATCCTGCTA ATGCTGTTT TAATGGCCTG CCAGTCTGGA	420
TTTGTCTTTG GCAACCAAAC AATTTGCTT CACAAGATTCTACTTAAGG GAAGAGAGGG	480
GCTCCTCATT TNTCACTTGT ACAAGAGCAG GGCTGGTCAG CTTTACACAG GTGTCAGATG	540
AACCGTCACA ANCCAGANTT NCATGTTGGC CTCAGGAGGG CTTCNAGGTC CAACATCTCG	600
ACGTAAGGAG CGTTCCCAGT TCTTCATGC TCAGATAACA GTNCTAACTN CAGCTGTTTC	660
ATCCCNAATC CCTANTTGAG GTCTTAACAT CTATTCCATT TTKCCNACMA GGGTTATNCT	720
GTAAACCCTC TNCACCAGAN TTAGANCTGA CTGATNCACT TCCTAG	766

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TCATACTTGT ATAGTTCKNT AAGATAATCA CTCTCTCACT CAGACATNNNG GNGRARNGCC	60
CNTCGATCAC TTGGGANAGG NGACTTGCMA TGTTAATGA TTGTCANCCM NANAANTAAAG	120
CTNACAGGGC AAAAACAGCC TYANGTCAGT TCTNTCTCCC TAATCCTCTA GAKNAAATC	180
NNAWRNTRNN ACTCTGNNTC TGTGCCATNA NANATNTTNC ANTTGTATTT ATGNACTCCA	240
CATNGAGTAC ACCTCACTAA WTNTNCTNCT GGGNAACNCC CSCMCCANTT TTTNNTTGNT	300
GANANACARC AATGCTGGCA TACNGTG	327

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCAGACTTTC ATAACNTGT TTATTATGAA GATTAGAGTN CTGAAGCTTA CTGGATTAGA	60
AGAGNACGAG GGGTAGCTG CCCAATATA TTCTAATTTC TCTKGAGGAC CACCAAATNG	120
GMAGAGTGTGTC TCTGATAGGG AAAAGGAAGA GTTGGAAAGGN ATCTTAGCCT CTAGGANAAA	180
AGAACCCATT TTATTGGCCA CCAAAGTTAC ATCTAGTKGC CTACAAATT ATNTCCAAAC	240
TCCTTATCCT GCCAATTCAAG GGTCTGNAA ACTGATGCCA AACTATAGTT TAGTCTNCTA	300
TCACATGACT GCATTATACA TACCCAATTA TCTGGGMAAA CAGACCTGAT CCAAACACAG	360
TTKGGTNCTT TCCTTNCCTT NCCTTKGTTT AGCCTGTYCC GTCTACTNNG GGTGTCTKG	420
ATTTGCTCCA G	431

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 276 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTTTTCCA CCAGACTTAC CAAATTTAG ATGNATGGAA GAACTGTAAA TNCCCATAAA	60
GNTAATCTAT NCATNGACCC CCACCATTAT GATAGAGATC ATNTGGTGAN TAATGAAAGA	120
TGAAACTCTC AGCTGGAAA GTAANAAGGA ATAGGATGTA AGTATGAGCT CCTGTTTTT	180
ATTATNTTTA TGGATGCCCT CTCAGAAAAA TATGNAANGG GGTAACTGAC TNNGAAATGG	240
GTNTTTTATG NATAGTAAGT CCCACTCACG AGGTTT	276

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCGAGATCTA AAGCAGATGN AGACTTTNCA CNAAATAAAT TTACTGCTTT TTYCTGTGA	60
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NATAAGTTNC GAGAAGGAAA GCTTTKGATT NCTRNATGAG TYCAGTGGAT TATYCTNAGN	120
ACTAGAGTKG NKGTKGAAGN CATGGNACAT TTATATAGWT YWTTCAAGTTC TACACTAAAT	180
GATGGAAGAA TGAGAAATCC TATATGACAA ATAGAAAAGT YCATYCTYCA TAATTGAGAA	240
CATTGAGCAG TTGGATTACC AAGATCTCGA	270

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTAGTTTA GACTAGTTTC ATTATACTAC CAGTTCTAA TATGTTGGTT TTTTATTAC	60
TATTTGATAT ATTTGTTTA ATATATGTTTC TTGTTTAGC AGGTAAAAGA ATCATAACAA	120
ATGTTTTAA AAGAACATTA TTATTCTTTA ATAACGTCT TTTTATGCAT TTGGCATGCC	180
AACTTTTTC ATTAACATCT TGGGTATTTT ATAAAAAGAG GGAAAGCTCA ATGTTAACAA	240
GGTAGCTTTT CTTAGGAGCT AAATTAATAA TTTAACAAAT CTCCTCCCT TCNCCTTCC	300
CCATCCCTCA AAGNATGGGT GNANTTATCT TTAACCTTTG GGCTNGCATC CNTGNAAGCT	360
TATGGNTANT CATAGTCTNA CMAAACTAGG GTCACCNAAC TTGGCAGCAG AAATAATCTA	420
GTCTTACTGT GATAACTACC CAATTACTTT ATTATTTTTC CAGTTNCAGT TCCAAATGTT	480
TTGTGGNAAN AATTTTNCT GTTTGTGATT TTCCAAGCTT AGAGGGGGAA ACCAACTTTC	540
CAGTGTGGA GAGCACTGNA TAGTTATGN ATTGTGTAAA	580

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGTTTCTTAA NACAGAAAAA AATTTACTGA TNGGACATTG TTCTAAGTGT ATTATTGTAT	60
TAAATGGATC ATTTAATTAA ATCTTCATAA CTGACATAGG AGTTGAGTAA CTTGTGTGGT	120
CAAATAGCTA GTAAGTGATG AGTAGGCTGG GCGCAGTGGC TCAAGCCTGT AATCCCAGCA	180
CTCTGGGAGG CTGAGGCAGG CAGATCACTT GAGGTCAAGGA GTTTGAGACC AGCCTGGNCA	240
ACATGGNAAA ACCTCGTCTC TACTAAAAAT ACAAAAATTA GCTGGCGTG GTGGGNGCGC	300
ACTTGTAGNC CCAGNTACTC GGAAGGCTGA GGCAGGAGGA ATCGCTT	347

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 430 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCACACAGN	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGN ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAAGCCAA ACTAAATCA CAGAGGGCAA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTTAATTTC TTTCAAAGTA GTTTTACTTA TTTNCAGATT CTATTTCTTT	300
ACTAGAATTAA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACAAAACAAA	360
GCTAGGTTTT NTNCATAGGT CTNCTTCCNN ATTGAATGAA CGTCTNTCCT CAAATTANC	420
CCCCCAGGGAA	430

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CAAACCCCTAT GNGAAATGGA AAGGAAACTA TTCTAAAGCA TAAAAGGTAG AAATATATAT	60
ACCACCCATC AAGAAAGATT ATTTTGNTG AACTCAAGTC ACCAGAGTGG CTAAAGCCCA	120
GTAGAATGGA AATGATTATA TGGAAGGTGA GGCCAAACGGG ACCAGAACAT ACTGTGATAG	180
ACAGNAAGGA GCTGTCTATC TTCTATTCTC CCACAGAAGG AGGTGACTAA GTCANCTGCC	240
CAAGCAATGT TATATCTGCA ATTGATGTNC AGCAGTACAA GTCTGAACAA CTTGGATTGG	300
NTGATTAATG TCCACANTAA ACATACAAGT CNTAATAGCT ATCTCTATAT AGTCTTTGGG	360
TNTTACAAG GCACTGNCAC ATNATCTCAC CTATTCCTCC	400

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGNATCCAGA ATTGAGTGNA GNGTTCTCTG GNCCACAGTC TCGGTATCTN CTGTGAAATG	60
GGGTATAGAT TCTACAATAA AACAAACACA NNNGCCCTAG GTCAGTGTAA ATGGAGATCA	120
CCANCCACAT TACCACCTCC AACACAGAAT TTTCTTTTC TTAATNCAAT NCGTNTCTTA	180
TAAGTCACTT TNCCCCAACT CACCAATCTA GNTAAGAATT TTTACCCCTGA GAAAAACAGC	240
TACACTCTAA AATTGCTNCA AAGAAAATGT CTAACATNTG GAAAGAAGGA CTTAACATGT	300
GANGNAGACA CTGGCTCCAT CTAGNGGGTG CTTTNTTTG AAATAATTAT AATNCCNCAT	360
CAAATTTNG GGGGNTACAG CTTATTAGGA ACTTGTATA GAACCAGATT CTGCCACAGA	420
ANCCACGTGG GTTGACAAGT GGTTGNCAGA AGAAAGGTAA TATGGCTTAT NATTAGGGNC	480
TCNCATCTGC AGAGTAATTG	500

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAATGCTTG ANNCAAATGT CATCTAGTTC CATCTCTACG ACTCTCATGG GGTCCAAAGA	60
AGAGTTTAN TTGAGTTTA GAATGTGAAG TTGTGAAGTG TCTGAAAAC TACATGGTGN	120
TCTGAAAGNC AAACCTTTAG CCTTGGGGGA GAGCATCTAA GACAGNAGGT GAAGGGNAGG	180
GGTTAGAACT AGAGGGATTG AAGAATATTA TCCATATAGG TTAGGGTTAG GTNNGGCAAC	240
GTTTATAGA ACAAACATTG GCAAGCTACA GCCACAGGCC AGATCTGTCT NCTACCTTCC	300
CACAAAGGTG TAATAACAAA GTTATTACACA AATGTGTGAA TAAACTNNCA TTGGAAAGTG	360
CCCACGCTCC TNGGTTATA CATTGTCTGT GGCTGCTTTC ACACACAGT AGCACAGGTG	420
AGTGTNTGCA CTGGAGACCA TATGCCCAT AGAGCTTAA	460

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 370 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATCAAGCAAC AGTGTGTTAT GCCTATACTC CATGTTATA TGTGTGTATT AAAAAATGTA	60
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TTTGTATATA TGTGTATGTA TAAAGTGTGTG TGTGTGTATG ATGATTCTNC TCCCGNTTTG	120
AAGGTGAAAG AAAGCACACC TTTATTTAAG CATAAACTTT GGGTTTCAGA TACTGTCTGG	180
AAAAATGATT TATCTCCAC TTTGAAATTC CAAAATACGT ACATATATTT TTTTTTCTT	240
TTCTTTTTA GTTTNAGGGT CTTGCTGTGT TGCCCAGGCT GGAGTGCAGT AGTGTGATCA	300
TAGNTCACAC AGNCTCTAAC TCCCAGGNTC AAGNTATCTT CCTGCCAG NCTCCTGAGT	360
AGNTGGGACT	370

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAAAAAATCA AAGGGAAGNT GGAACCCCTG CCCACCTCTC CATTCCCCAT TCTGCTGGTG	60
GTGNCTGCTC TTCCTCACAG TACCTCCTGA AAAGTTCAGA ATTCAAGTAA TACAGAATTA	120
TTGGGTTGAT TTTCAACGTG TAGTTAAGA TGAAGAGTTC CGNTTGGTTT AAACCACCTTC	180
ACCTAACCTC TTGGTAACGG TAGTCCTGAG AGTCGCAGT GTCANTGAAA ATCGTCCTGT	240
GACCACGCGT CAAGCTGCTG ATGGGGGACA GAAACTTCCG GGNCTATCAT ATCTCCTTGA	300
NCTCGGCCCT CAAATCTGGT AGTTTCTGCA CCGAGGGACA CAGTCCACTG CGATGAAGTA	360
TGTTCAAAAT CGNTTCTTT AGGGAACTCC TTCCAAAGTC CAATAGTGNA AGGTGGTCAA	420
GGAAGGATTG GGAAGGAAGN TGNAAAAGTC AGNCGGGAAAT CTTGATTTGG NTAGNTGTGG	480
ANANAGGAAA TCACTTGGCC	500

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGAAAGAGGT CTCCTAACAC CCAGACAGTG TAAAAATCCA GTTTTCTTC CTTTGGNNG	60
GAGACAGAGT CTCGCACTGT AGCTCAGGCT GGAGTGCAGT GGCAC	105

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AGTCCCAGCT ACTCAGGAGG CTGGGGCAGG AAGATAGCTT GAGCCTGGGA GTTAGAGGCT	60
GTGTGAGCTA TGATCACACT ACTGCACTCC AGCCTGGCA ACACAGCAAG ACCCTAAAAC	120
TAAAAAAAGAA AAGAAAAAAA AAATATATGT ACGTATTTG GAATTCAAA GTGGGAGATA	180
AATCATTTC CCAGACAGTA TCTGAAACCC AAAGTTTATG CTTAAATAAA GGTGTGCTTT	240
CTTTCACCTT CAAAGCGGGA GAAGAACAT CATAACACACA CACACACTTA TACATACACA	300
TATATACAAA ATACATTTT TAATACACAC ATATAAACAT GGAGTATAGG CATAACACAC	360
TGTTGCTTGA TAAAATATAG GGATCC	386

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TATATTTNAT CAAGCAACAG TGTGTTATGC CTATACTCCA TGTATATATG TGTGTATTAA	60
AAAATGTATT TGTATATATG TGTATGTATA AGTGTGTGTG TGTGTATGAT GATTCTCCTC	120
CCGNTTGAAG GTGAAAGAAA GCACACCTTT ATTTAACAT AAACTTTGGG TTTCAGATAC	180
TGTCTGGAAA AATGATTTAT CTCCCACTTT GAAATTCCAA AATACGTACA TATATTTTT	240
TTTTCTTTTC TTTTTAGTT TNAGGGTCTT GCTGTGTTGC CCAGGCTGGA GTGCAGTAGT	300
GTGATCATAG NTCACACAGG CTCTAACTCC CAGGNTCAAG CTATCTCCT GCCCCAGNCT	360
CCTGAGTAGG TGGGACT	377

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CTGCAGTAAG CCACGTTCAT GCCACTGTAC TCTAGCGTGG ATGACAGAGA GAGATCCTGT	60
CTTTGGAAGA AAAAAACAAA AAGAAAAAAA AAAGAGTATG GCCATGGCCT TATAATATAG	120
AAGGGGTACAC ATATTAATCT CTGAAATGG ATCTCTTGTG GGCTTCATA CAAGGCAACA	180
GCCACAGAGT ACGTACCTGA AAGCTGCCTG GGNTTAATGG CTGGNAGTAT GTTCTAACTN	240
GTTCAGGNAC CCATGTCACN ACTGGTGGTT ACAGAATGTG AATCTCACAC TGTCCNAAAT	300
CGGTTTATT TTTAAAANGA ATAATTCTAN TACATTACCT TATAAAAAGT AGGTAACCTA	360
ATTTGGNTT TTAAAAGTGA ATTGAGGGCA GATGCAAGTG GNTCACACCT ATTAATCCCA	420
AATACCTTGG AGAGGGCAAG GTAGGAGGAT TGGTTGGAGC CCAGGAGTCC AAAGACCAGG	480
CTAGGGAATA TTGNAAGAAN GTCCTCTCTA CAANAAAANAA T	521

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTGCANGAAG CTTTTNTTNC TTTTNGGNGG AGACAGAGTC TTGCTGTGTC ANCCCAGGCT	60
GGGGTGCAGT GGNACAGTCA TAGCTCACTG CAACCTTGAA CTCCCTGGNT CATGCGATCC	120
TCCCACCTCA GCCTCTCAAG TAGCTAGAAC TACAGGTGTG CACCACCATG CCTGACTAAC	180
TTGTTTATTN GNGGGAGAGA GAACGNTCTT GCTATATTGC CTAGGCTGGT CNTTGAACTC	240
TTGGGNTNCA AGCAATCCTC CTACCTTGGC CTCTNCAAGG TANTTGGGAT TNATAGGTGT	300
GAGCCACNTG CATCTGGCCT CAATTCACTT TTAAAATNCA AAATTAGGTT ACCTACTTTT	360
TATAAGGTAA TGTATTAGAA TTATTCTNN NAAAAATAAA ACCGATTTGG GAAAGNGTGA	420
GANTCACATT CTGTAACCAC CAGTGGTGAA ATGGGTCCCC GAACAAGGTA GAACATACTC	480
CCAGCCATTA ACCCCAGGGA GNGTTCAAGT CCGTNC	516

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATCCTGTT TCTTAAAACA GAAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
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TTGTATTAAA TGGATCATT	AATTTAATCT TCATAACTGA	CATAGGAGTT GAGTAAC	TTG	120
TGTGGTCAAA TAGCTAGTAA	GTGATGAGTA GGCTGGCGC	AGTGGNTCAA GCCTGTAATC		180
CCAGCACTCT GGGAGGCTGA	GGCAGGCAGA TCACTTGAGG	TCAGGAGTTT GAGACCAGCC		240
TGGCCAACAT GGNAAAACCT	CGTCTCTACT AAAAATACAA	AAATTAGCTG GGCGTGGTGG		300
GTGCGCACTT GTAGTCCCAG	CTACTCGGAA GGGTTGAGGC	AGGAGGAATC GCTTGGTCCC		360
CGGGAGGGAG AGGTTGNTNG	TGNAGCTGAG ATCACGCCAC	TNGCACTCCA GGCTGGNAA		420
CAAAAGGGAG ACCTTNCTC	AAAAAAAAAT NAAAATAAAA	AGTGATGAGT AGGATTGGGA		480
CCCNAGACAT CTTTCTCCA	AGACC			505

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGCAGNCTC AAACCCTTGT	CCTGGGATCA AACAACTCTC	CCACCTCAGC CTTCAAAGTA		60
GATAGAACTA CAGGCATGCA	CTACCATGCC TAATTTTTA	AAAAAAAAATT TTTTTTCAGA		120
GATGAGATCT CACTGTGTTT	CCCAGGNTTG TCCGGAAC	TCCTCAA GCGATCCTCC		180
CACCTTGGGC TGCCAAAGTG	TTGGGATTAC AGGCATGAGC	CACCATGCCT GGCCATACAC		240
TTTTTTTTTT TTTTAANCA	AGACGGAGTC TNGTCTGTC	GCCCAGACTG GAGTGCAGGG		300
GCGTNNATCT TGGCTCACTT	GAAAGCTTCG CCTCCCAGGG	TTCATGCCGT TCTCCTGNCT		360
CAGCCTCCCA AGTNGGTGGG	ACTACAGGNA TCTGCACCAC	GNCCGGTTAT TTNTTGGGTT		420
TGNNGNAGGG ACGGGGTTTC	ACCATGTTAG GCAGGATGAC	TTCGGACTTC CNGACCCAAG		480
ATCACCCCTGC TCGGCTCCCA				500

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCAGA CGAGCCTGGG	CAACACAGTG AGACTCTATC	ACTACAAAAA AATTTTAAAAA		60
TTAGCTAAAG TTGATGGNAC	ATGCCTGCAG TCCCAGCTAC	TCAGGAGGCT GGGCAGGAA		120
GATAGCTTGA GCCTGGGAGT	TAGAGGCTGT GTGAGCTATG	ATCACACTAC TGCACACTCCAG		180

CCTGGGCAAC ACAGCAAGAC CCTAAAAC TA AAAAAGAAAAA GAAAAAAAAT ATATATGTAC	240
GTNTTTGGGG AATTCAAAG TGGGAGATAA ATCATTTC CAGACAGTNT CTTGAAACCC	300
AAAGTTTATG CTTAAATAAA GGTGTGCTTT CTTTCACCTT CAAANGCGGG AGAAGGATCA	360
TCATNCACAC ACACACACTN ATCATNCACA TTTTACAAA TNCAATTNNN NAATACAACA	420
CATTTAAC A TGGGGTTTG	440

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATCCTGTT TCTTAAAACA GAAAAAAATT TACTGATAGN ACATTGTTCT AAGTGTATTA	60
TTGTATTAAA TGGATCATTT AATTAAATCT TCATAACTGA CATAGGAGTT GAGTAACCTG	120
TGTGGTCAAA TAGCTAGTAA GTGATGAGTA GGCTGGCGC AGTGGCTCAA GCCTGTAATC	180
CCAGCACTCT GGGAGGCTGA GCCAGGCAGA TCACTTGAGG TCAGGAGTTT GAGACCAGCC	240
TGGCCAACAT GGNAAAACCT CGTCTCTACT AAAAATACAA AAATTAGCTG GGCGTGGTGG	300
NTGCGCACTT GTAGTCCCAG CTACTCGGAA GGCTNGAGGC AGGAGGAATC GCTTGATCCC	360
NGGGAGGGAG AGGTTGGTNG TGANGCTGAG ATCACGNAC TTGNACTCCA GNCTGGNAA	420
CAAANGNGAG ATCTTNTCTC AAAAAAAAAT AAAANTAAAAA NGTGTGAGT AGGATTTGGA	480
CCCCAGACAT CCTNTCTCCA GGACCTGGNA TTC	513

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCCCTGG NCTCAAGTGA TCCTCTCACC TCAGCCTCCC AAATTGCTGG GATTAGAGTG	60
TGAGCCACTG TGCCTAGCCT GCATATATCT ATTTTAATG ACTGCTAAAT CTCATTGTAT	120
GAAAATTTAT GTCCTAGCTA TAAAATTGN TAGCACATGT TTAATTTTT CTAATTCAG	180
ATGTTTTAAA CTAATATTTC CCAAAGTATA GTATGGCATT TTAGGTATGA TATGATCTT	240
NNTCCTCTTC GTACTCATTT TTATAGTTAT GGCCTGTGCA ACTGGTTCC CATTATATG	300

AATGATACAG AGCTTCCTAT TAAGAAAAAG TTCAGCTTGG GGAAAAAAAAGTGAATTGT	360
CAACTTNGAG GGAAAAAAGT GAATTATTGG	390

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTTCA GTATATGGTA	60
AAACCCAAGA CTGATAATTT GTTTGTACACA GGAATGCCCG ACTGGAGTGT TTTCTTTCT	120
CATCTCTTTA TCTTGATTTA GAGAAAATGG TAACGTGTAC ATCCCATAAC TCTTCAGTAA	180
ATCATTAAATT AGCTATAGTA ACTTTTTCAT TTGAAGATTT CGGCTGGGCA TGGTAGCTCA	240
TGCCTGTAAT CTTAGCACTT TGGGAGGCTG AGGCGGGCAG ATCACCTAAC CCCAGAGTTC	300
AAGACCAGCC TGGGCAACAT GGCAAAACCT CGTATCTACA GAAAATACAA AAATTNGNCG	360
GGNATG	366

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AACACCAGGG NCATGAGGGC ACTAATCATA ATGAGATATG CCTGCTGGAG TCGAAGTGGA	60
CCTTCCAGT GAATGGAAAT CATTCCCACC ACACCAAAAT TCCAGATCAG GAGTGNAACA	120
GTAATGTAGT CCACAGCAAC GTTATAGGTT TAAACACTT CCCTGAAAAAA AAATTACACA	180
GATTTAAAAA GATGTACAAT AATTCCACC AAAACATTAT TTAGAATAAT GTGATGGCTC	240
CCAAACATTA GATATTAATN TCCCACCTT ATAATTTAC CATAACCTAT ATCAACTGTG	300
CTATTATTTA TTTAATNCTT CCCTNTAAAT TAATTTACTC TTTTTTGTG TTTGTTTTG	360
NGTTGGAGC CAGTGTCTCA TTTGGTTGC CCAGGCTTGG AGTAAAGTGG GTGCAATCAC	420
GGCTCAACTG NAGTCTTNC CTCCNGGAGA TCAGGTNGGT CTTCCCCAGG TCCAANCTCC	480
TAAGTTGGTT NGGANAAC	498

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TAAACAAACAG GGNCATGAGG GCACTAATCA TAATGAGATA TGCCTGCTGG AGTCGAAGTG	60
GACCTTTCCA GTGAATGGAA ATCATTCCCA CCACACCAAA ATTCCAGATC AGGAGTGAAA	120
CAGTAATGTA GTCCACAGCA ACGTTATAGG TTTTAAACAC TTCCCTGAAA AAAAATTACA	180
CAGATTTAA AAGATGTACA ATAATTCCA CCAAAACATT ATTTAGAATA ATGTGATGGC	240
TCCCCAACAT TAGATATTAA TNTCCCACCT TTATAATTTC ACCATAACCT ATATCAACTG	300
TGCTATTATT TATTTAATNC TTCCCTCTAA ATTAATTAC TCTTTTTTG TTTTGTTTT	360
TGTGTTGGA GCCAGTGTCT CATTGGTT GCCCAGGCTT GGAGTAAAGT GGGTGCAATC	420
ACGGCTCAAC TGNAGTCTT ACCTCCGGA GATCANGTTG GTCTTCCC	469

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 370 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GT TTATCAAG TACCTCCCTG AATGGACTGN GTGGCTCATC TTGGCTGTGA TTTCA GTATA	60
TGGTAAAACC CAAGACTGAT AATTTGTTTG TCACAGGAAT GCCCCACTGG AGTGT TTCT	120
TTCCCTCATCT CTTTATCTTG ATTTAGAGAA AATGGTAACG TGTACATCCC ATA ACTCTTC	180
AGTAAATCAT TAATTAGCTA TAGTAAC TTT TTCATTGAA GATTTCGGCT GGGCATGGTA	240
GCTCATGCCT GTAATCTTAG CACTTGGGA GGCTGAGGCG GGCAGATCAC CTAAGCCCAG	300
AGTTCAAGAC CAGCCTGGGC AACATGGCAA AACCTCGTAT CTACAGAAAA TACAAAATT	360
AGCCNGGNAT	370

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTCATGGTGT TGGCGGGGAG TGTCTTTAG CATGCTAATG TATTATAATT AGCGTATAAGT	60
GAGCAGTGAG GATAACCAGA GGTCACTCTC CTCACCATCT TGGTTTGGT GGGTTTGGC	120
CAGCTTCTTT ATTGCAACCA GTTTTATCAG CAAGATCTT ATGAGCTGTA TCTTGTGCTG	180
ACTTCCTATC TCATCCCGNA ACTAAGAGTA CCTAACCTCC TGNAATTGA AGNCCAGNAG	240
GTCTGGCCT TATTTNACCC AGCCCCTATT CAAAATAGAG TNGTTCTGG NCCAAACGCC	300
CCTGACACAA GGATTT	316

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGCAGNCCG GGGGATCCTG GTAAAAGTCA CAAGGTCAGC CTACTAAAGC AGGGAAAACT	60
AAAGGCAAGT AAACACGTGC AGACAAAAAA AGGGATAAAAG AAAAGGAATT AAGAAACTAG	120
CATTTTTAAN GTGGGGGAGG TGAATGCTTC CCAGAATGGG TTTATATCAC TTGCTTGNNG	180
GCCTTCTGAG TGTTGGNAAC AACCTGTCAT CATCACACAT ACCTGTCATC TTTAATGGTC	240
TCCATACATT ACTAATAGAT TATACAGATG GCCATCACTT AACACTTCCA CTCACTCAAT	300
TTGTNCAACA TGCAAGGTTA CCCTCTTTT TNGCTTACNG CCACAAAGCA TTGGANAAGG	360
TTTGTGATTT TTACTAGCCN CCACTTCATC AAATTTAAGC ATTTCTTTT TCCTNTTAAC	420
ANCCAGGACA GGNTTNAACN AAGGAAAT	448

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGCAGCTCC AAGCACCTTT TCACAAATTCA GCTTTCTGTG ATTCAGACC ACATATGCAA	60
GGAACATATCT TACCTTAATT AATAAGACTT TAAAATCCTT GTGTCAGAGG CGTTTGGACC	120
AGAGCAACTC TATCTTGAAT AGGGGCTGGG TAAAATAAGG CCAAGACCTA CTGGGCTGCA	180
TTTGCAGGAG GTTAGGTACT CTTAGTTACG GGATGAGATA GGAAGTCAGC ACAAGATACA	240

GCTCATAAAG GATCTTGCTG ATAAAACCTGG TTGCAATAAA GAAGCTGGNC AAAACCCACC	300
AAAACCCAAGA TGGTGAGGAG AGTGACCTCT GGTTATCCTC ACTGNTCACT ATACGNTAAT	360
TATTATACAT TAGCATGCTA AAAGACACTC CCCGCAACAA CCATGANAGG TTTACAAGTT	420
NCCATGGNAA CGNNCCCGGA NGNTANCTTG	450

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 388 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGNAGCCTC CACCACCCAG GTTCAGGTGA TTCTCCTGCC GTAGNCTCAT GAGTAGNTGG	60
GATTACAGGC ATGTGCCACC ATGCCCGACT AATTTTATA TTTTTAGTAG AGACGGGGTT	120
TCACCATGTT GGGCAGGCTG GTCTCAAACCT CCTGACCTCA AGTGATCTGC CCACCTTGGC	180
CTCCCAAAGT GCTGGGATTTC CAGGCGCCTG GCCTGTTACT TGATTATATG CTAACAAAGG	240
GGTGGATTAT TCATGAGTTT TCTGGAAAG AGGTGGGCAA TTCCCGGAAC TGAGGGATCC	300
CTCCCCTTNN NAGACCATAAC AAGGTAACCTT CCGGACGTTG GCATGGNATC TTGTTAAACT	360
TGTCATGGNG TTGGGGGGGA GTGTCTTT	388

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CTGCAGAAAGT ATGTTCCCTG TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA	60
ACACATAAAAT TCTTTCCAC CTCAGGGNCA TTGGGCGCCC ATTGCTCTTC TGCCTAGAAT	120
ATTCTTTCCCT TTTCTAACTT TGGTGGATTAA AATTCCCTGTC ATCCCCCTCC TCTTGGTGT	180
ATATATAAAAG TTTTGGTGCC GCAAAAGAAG TAGCACTCGA ATATAAAATT TTCCTTTAA	240
TTCTCAGCAA GGNAAGTTAC TTCTATATAG AAGGGTGCAC CCNTACAGAT GGAACAATGG	300
CAAGCGCACA TTTGGGACAA GGGAGGGGAA AGGGTTCTTA TCCCTGACAC ACGTGGTCCC	360
NGCTGNTGTG TNCTNCCCCC ACTGANTAGG GTTAGACTGG ACAGGCTAA ACTAATTCCA	420
ATTGGNTAAT TTAAAGAGAA TNATGGGGTG AATGCTTGG GAGGAGTCAA GGAAGAGNAG	480

GTAGNAGGTA ACTTGAATGA

500

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CTGCAGAGTA ATTGCAACTG GAGTTGTCTT AAGATAATGT CACATATCCA TCTTCCCCTT	60
GTTTCTCATT CACAGAAAAA CATTTTTATT CCAGGTGCCA ATATTCCCAG CCAAAAAGAC	120
TTTACTTCTG ACTCCCTTAT ATTTAGGATG GCTATGAGAA CAAGTAAGGG CAATGACTTC	180
TAGGGAGATG TGTTGTGTAT GGAACCTCTA AGGAGAGAAT TCTGCTGACA TGTCCATGT	240
TCTTTCTCC CCTACTCCTT CCTACTGTCA GAAATGAAGG CTAGGGCTCC AGCCTGGACC	300
CTGAAGTAAG CTAGAGGTTA GAAGCTAAAG AAGAAAGAAG GAGATTGAGT CCTTGGATGA	360
ACGTGAAGCC ACCCTACTAA TCTGGACTGN CTACCTCTGN ACTACTCTAT GAGAGAGAAA	420
GTATGTGCAT TATTT	435

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 439 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CATGCTCTTT GTCCCTGTGA CTCTCTGCAT GGTGGTGGTC GTGGNTACCA TTAAGTCAGT	60
CAGCTTTTAT ACCCGGAAGG ATGGGCAGCT GTACGTATGA GTTTGGTTTT ATTATTCTCA	120
AAGCCAGTGT GGCTTTCTT TACAGCATGT CATCATCACC TTGAAGGCCT CTGCATTGAA	180
GGGGCATGAC TTAGCTGGAG AGCCCACCT CTGTGATGGT CAGGAGCAGT TGAGAGAGCG	240
AGGGGTTATT ACTTCATGTT TTAAGTGGAG AAAAGGAACA CTGCAGAACT ATGTTCTG	300
TATGGTATTA CTGGATAGGG CTGAAGTTAT GCTGAATTGA ACACATAAAAT TCTTTCCAC	360
CTCAGGGGCA TTGGCGCCC ATTGNTCTTC TGCCTAGAAT ATTCTTCCT TTNCTNACTT	420
GGGNNGGATTA AATTCCGT	439

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 318 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCCATCTCTA CGACTCTCAT GGGTCCAAA GAAGAGTTT AATTGAGTTT TAGAATGTGN	60
AGTTGTGAAG TGTCTGAAAA ACTACATGGT GNTCTGAAAG NCAAACTTTT AGCCTTGGGG	120
GAGAGCATCT AAGACAGNAG GTGAAGGGGA GGGGTTAGAN CTAGAGGGAT TGAAGAATAT	180
TATCCATATA GGTTAGGGTT AGGTGTGGCA ACGTTTATA GAACAAACAT TGGNAAGCTA	240
CAGACACAGG CCAGNTCTGT CTNCTACCTN TCCACAAAGG TGTNATAACA AAGTTANNCA	300
CAAATGTGTG AATAAACT	318

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTGCAAAGT CATGGATTCC TTTAGGTAGC TACATTATCA ACCTTTTGA GAATAAAATG	60
AATTGAGAGT GTTACAGTCT AATTCTATAT CACATGTAAC TTTTATTGGA ATATATCAGT	120
AATAGTGCTT TTTCNTTTTT TTTTTTTNTT TTTTTNNNTT TTNGGGANA GAGTCTCGCT	180
CTGTCGCCAG GTTGGAGTGC AATGGTGCGA TCTTGGCTCA CTGAAAGCTC CACCNCCCGG	240
GTTCAAAGTGA TTCTCCTGCC TCAGCCNCCC AAGTAGNTGG GACTACAGGG GTGCCGCCACC	300
ACGCCTGGGA TAATTTGGG NTTTTTAGTA GAGATGGCGT TTCACCANCT TGGNGCAGGC	360
TGGTCTTGGGA ACTCCTGANA TCATGATCTG CCTGCCTTAG CCTCCCCAAA GTGCTGGGAT	420
TNCAGGGGTG AGCCACTGTT CCTGGGCCTC	450

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 489 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CTGCAGNTGA GCCGTGATTG CANCCACTTT ACTCCNAGCC TGGGCAANCA AAATGAGACA	60
CTGGCTNCAA ACACAAAAAC AAAACAAAAA AAAGAGTAAA TTAATTAAA GGAAAGTATT	120
AAATAAATAA TAGCACAGTT GATATAGGTT ATGGTAAAAT TATAAAGGTG GGATATTAAT	180
ATCTAATGTT TGGGAGCCAT CACATTATTC TAAATAATGT TTTGGTGGAA ATTATTGTAC	240
ATCTTTAAA ATCTGTGTA TTTTTTTCA GGGAAAGTGT TAAAACCTAT AACGTTGCTG	300
TGGACTACAT TACTGTTGCA CTCCTGATCT GGAATTTGG TGTGGTGGGA ATGATTTCCA	360
TTCACTGGAA AGGTCCACTT CGACTCCAGC AGGCATATCT CATTATGATT AGTGCCCTCA	420
TGGCCCTGGT GTTTATCAAG TACCNCCTG AATGGACTGG GTGGCTCATC TTGGCTGTGA	480
TTTCAGTAT	489

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CTGCAGNCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCACC ATGCCCGGCT AATTTTGTA TTTTCTGTAG ATACGAGGTT	120
TTGCCATGTT GCCCAGGCTG GTCTGAACCT CTGGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGC ATTCTGTGA	360
CAAACAAATT ATCAGTCTTG GGTTTACNA TATACTGAAA TCACAGCCAA GATGAGCCAC	420
GCAGTCCATT CAGGGAGGTA CTTGATAAA	449

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGCCGT TCCCGACCCG AGCCTGGTGC CCCTCCCCA TTATGATCCT TNTCGCTTCC	60
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GGCGGCATCG	GGATGCCCG	CGTTGCAGGC	CATNCTGTCC	CAGNCAGGTA	GATGACGACC	120
ATCAGGGACA	GCTTCAGGA	TCGCTCGCGG	CTCTTACCAAG	CCTAACTTCG	ATCATTGGAC	180
CGCTGATCGT	CACGGCGATT	TATCCCGCCT	CGGCGAGCAC	ATGGAACGGG	TTGGCATGGA	240
TTGTAGGCGC	CGCCCTATAC	CTTGCTGCC	TCCCCCGCGT	TGCGTCGCGG	TGCATGGAGC	300
CGGNCCACCT	CGACCTGAAT	GBAANCCGGC	GGCACCTCGC	TAACGGATTC	ACCACTCCAA	360
GAATTGGAGC	CAATCAATT	TTGCGGAGAA	CTGTGAATGC	NCAAACCAAC	CCTTGGCAGA	420
ACATATCCAT	CGCGTCCGCC	ATCTCCANCA	GCCGCACGCG	GCGCATCTCG	GGCAGCGTTG	480
GGTCCTGCAG						490

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGCAGTGT	TAAAAAATAA	AATAAACTAA	AAGTTTATTT	ATGAGGAGTA	CACTGCTTTC	60
TTGTAAACAC	ATGTACAAGC	CATATAATAG	AGTTCATTT	NNACCCTAGT	TACGGAAACA	120
CTAGAAAGTC	TNCACCCGGC	CAAGATAACA	CATCTTCTAGG	TAAAAATAGC	AAGAAATATT	180
TTATGGGTTG	TTTACTTAAA	TCATAGTTTT	CAGGTTGGGC	ACAGTGGNTC	ATGCCTGTAA	240
TCCCAGCACT	TTATGCGGCT	GAGGCAGGCA	GATCAGTTGA	GGTCAGAAGT	TTGAGACCAG	300
CCTGGGCAAT	GTGGCAAAAC	CTCATCTCCA	CTAAAAATAC	AAAAATTAGC	CAGGCATGGT	360
GGTGCACACA	TGTTAATTCC	CAGCTACTTG	GGAGGNTTGA	GACAGGAGGG	TCGCTTGGNC	420
CTAGGAGGGA	AGAAGTTGNA	GGGANCTTAA	TGTCACTGCA	CTCTAGNTTG		470

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CACTCAATT	TGAATGCTGC	CATCATGATC	AGTGTCAATTG	TTGTCA	TGAC TANNCTCCTG	60
GTGGTTCTGT	ATAAAATACAG	GTGCTATAAG	GTGAGCATGA	GACACAGATC	TTTGNTTTCC	120
ACCCCTGTTCT	TCTTATGGTT	GGGTATTCTT	GTCACAGTAA	CTTAACTGAT	CTAGGAAAGA	180

AAAAATGTTT TGTCTTCTAG AGATAAGTTA ATTTTAGTT TTCTTCCTCC TCACTGTGGA	240
ACATTCAAAA AATACAAAAAA GGAAGCCAGG TGCATGTGTA ATGCCAGGCT CAGAGGCTGA	300
GGCAGGAGGA TCGCTTGGC CCAGGAGTTC ACAAGCAGCT TGGGCAACGT AGCAAGACCC	360
TGCCTCTATT AAAGAAAACA AAAAACAAAT ATTGGAAGTA TTTTATATGC ATGGAATCTA	420
TATGTCATGA AAAAATTAGT GTAAA	445

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CCTGTATTTA TACTGAACCA CCAGGAGGAT AGTCATGACT ACAATGACNC TGATCATGAT	60
GGCAGCATTG AGAATTGAGT GCAGGGCTCT CTGGCCCACA GTCTCGGTAT CTTCTGTGAA	120
TGGGGTATAG ATTCTACAAT AAAACAAACA CAAAAGCCCT AGGTCAGTGT TAATGGAGAT	180
CACCAACCAC ATTACCACCT CCAACACAGA ATTTCTTT TCTTAATTCA ATTGNATCT	240
TATAAGTCAC TTTTCCCCAA CTCACCAATN CTAGCTAAGA ATTTTAACC TGAGAAAAAC	300
AGCTACACTC TAAAATTGCT TCAAAGAAAA TGTCTAACAT ATGGAAAGAA GGACTTAACA	360
TGTGAAGCAG ACACGGCTC CATCTAGTGG GTGCTTATA TTGAAATAAT TATAATACCT	420
CATCAAATTG TTTNGGGTAC AGNTTATTAG GAACTGGTA TGGAACCAGA TTCTGCCACA	480
GAAACCACGN GGGCTG	496

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATTAGATAA TGGNTCAGGG TGGCCAAGGC TCCGTCTGTC GTTGTGCTCC TGCCGTTCTC	60
TATTGTCATT CTATAAGCAC AAGAAAAACA TTTTCAGTAA ATCAGATTCT CAGCAGAAC	120
AAGGTAACGG TTAGACCTGG GATTAACAAC AGACCCGTCA CTATGAGTTC TAAAAACCTG	180
AAGCAAGAAA AAACAATGTA CAGGAAGTAT GCAGTTAAA AGTCTAGATT ATCTATCATT	240
GTTCACTGAA GGCATTCAGG TCCTCTCTT TACCTGGTC TTGGNTTGCT CCATTCTCTC	300

TGTCATCCC AACATACACA ATTGTACTTA TCCTTGAGA TGTACCTTAA ATACTGACAC	360
CTGCATGAAA ACTTGTTCAC TGGCTGCAGG TCCAAGCACC TTTTCNAAA TTCAGCTTTC	420
TGTGATTCA GACCACATAT GCAAGGAACt ATCTTACCTT AATTAATAAG ANTTAAAAT	480
CCTTGTGTCA GAGGCG	496

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AGGANCGCTT GGGCCCAGGA GTTCACAAGC AGCTTGGCA ACGTAGCAAG ACCCTGCCTC	60
TATTAAGAA AACAAAAAAAC AAATATTGGA AGTATTTAT ATGCATGGAA TCTATATGTC	120
ATGAAAAAAAT TAGTGTAAAA TATATATATT ATGATTAGNT ATCAAGATTT AGTGATAATT	180
TATGTTATNN NGGGATTTCAT ATGCCTTTT AGGCCATTGT CTCAAAAAAAT AAAAGCAGAA	240
AACAAAAAAA GTTGTAAC TG AAAATAAAC ATTTCCATAT AATAGCACAA TCTAAGTGGG	300
TTTTGNTTG TTTGTTGNT TGTTGAAGCA GGGCCTTGCC CTNCCACCCA GGNTGGAGTG	360
AAGTGCAG	368

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 500 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCCTT TTTTTTTTTT TTTTTTTTT TTNCCTCAA TGTAAAAATT GTNCCTTAGA	60
TAACGGATA GNACAAAGTT NGNCTTNGTT TTTACTTAA AAAACGTACT TTCCGCATAC	120
TGTNGCCCGT ATGACTTTCC TGTCCCATCG GAAACCAGAG TTTCCCCAGG TGAGCCCTTC	180
CTATCTGNGG NTACATGATT TAGCTAATT AACAAAGAAGA GAGTAATTCC TTNGGATTAT	240
TATCAACATG AAACTGGAC TATGTCTCTA TAAGGGTGAA CACTGATT TTTTTCTTT	300
TTAGAAACAA AAACCATCCA CTTATTAATC CAAACTACGG GATTGGATT ACAACAATCA	360
TCGCATNAAC TGAACATACG AAGTTACCAc TCAAGGGAAT NACAGAAGAA CGTTGNACAA	420
TNTNTCTTAC GGGGTACGNG AATTCAAACA ATGTGGGGAN AGGAACCTCA NTCTACAAAN	480
TCTGACCATC GNTTCAGTAT	500

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCCCTT ACTCTTCTTT AATTCTACCG TCTTGGGCA TACATCTCAT TTGNTGTGGA	60
AGAAGGTCTG ACAGNAGGGC TGACAGCACC GATTCTAAC ACATTCTTT CATCATACAA	120
AGAGTAAGAC CCTAGAATAA TGGGACCATC TGCTACCACG ACAGAGCTGC CTTACTGGCT	180
GTAGAAAAAG ACTGCTTGTG TGGGAGAGAA GAATGAGGAC AGAGGAGGCA TCTGGGGCAA	240
GTGAGCGTAC AAGTATNTCT ACAAAATTCAAG AATTGGTGG AAAATCCAAA TTTGNCTTCA	300
ACATGATAGA GAATTGATGA GAAAATAGCT GTNCTGTTTC CAAAATTAC TGAATTGGG	360
AACCTGAGGT TAAAACCTTT AGGATNAAGC AACTCAGGTT CAAGACTTNG NCTNGGAAG	420
GAATGGAAAC ACAGACGGGA ATGAGTNTCA	450

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAACTGTATT TATACAGNAA CCACCAGGAG GATAGTCATG ACAACAATGA CAAACTAGGA	60
ATAGCCCCCT TTCACTTCTG AGTCCCAGAG GTTACCCAAG GCACCCCTCT GACATCCGGC	120
CTGCTTCTTC TCACATGANA AAAACTAGCC CCCAGTNTGA TCCGCAGGTN GAGGAATNCC	180
CCGGGTCGAG GTTCGGATCC TGGATGACAG ACCCTCTCGC CCCTGAAGGN GATAACCGGG	240
TGTGGTACAT GGACGGNTAT CACAACAACC GCTTCGNACG TGAGTACAAG TCCATGGTTG	300
ACTTCATGAA CACGGACAAT TTCACCTCCC ACCGTCTCCC CCACCCCTGG TCGGGCACGG	360
GGNAGGTGGT CTNCAACGGT TCTTTCTNCT TCAACAAGTT CCAGAGCCAC ATCATCATCA	420
GGTTTGGACC TGAAGANAGA GAACATCCTC	450

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GGATCCCTCC CCTTTTCTAGA CCATACAAGG TAACTTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGAGCAG TGAGGATAAC CAGAGGTAC C TCTCCTCACC ATCTTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGTAACTAAG AGTACCTAAC CTCCTGCAAA TNGCAGCCCA	300
GTAGGTCTTG GNCTTATTTT ACCCAGCCCC TATTCAAGAT AGAGTTGCTC NTGGTCCAAA	360
CGCCTCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGGT CCTTGGATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTTG GAAAAAGGTG CTTGGAGCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT	500

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CTGCAGTGAG CCAAAATCGT GCCACTGCAC TTCACTCCAG CCTGGGTGAC AGGGCAAGGC	60
CCTGCTTCAA CAAACAAACA AACAAACAAA AACCCACTTA GATTGTGCTA TTATATGGAA	120
ATGTTTATTT TTCAGTTACA ACTTTTTTG TTTCTGCTT TTATTTGTT AGACAATGGC	180
CTAAAAAGGC ATTGAAATNC CAAAATAACA TAAATTATCA CTAAATCTTG ATAACATAATC	240
ATAATATATA TATTTTACAC TAATTTTTC ATGACATATA GATTCCATGC ATATAAAATA	300
CTTCCAATAT TTGTTTTTG TTTCTTTAA TAGAGGCAGG GTCTTGCTAC GTGCCAAG	360
CTGCTTGTGA ACTCCTGGGC CCAAGCGATC CTCCTGCCTC AGCCTCTGAG CCTGGCATT	420
CACATGCACC TGGCTTCCTT TTTGTNTTT TTGAATGTTC CACAGTGAGG AGGAAGAAAA	480
CTNAAAATTA ACTTATCTCT	500

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 450 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CTGCAGATGA GAGGCACTAA TTATAAGCCA TATTACCTTT CTTCTGACAA CCACTTGTCA	60
GCCCCACGTGG TTTCTGTGGC AGAATCTGGT TCTATAACAA GTTCCTAATA AGCTGTAGCC	120
AAAAAAATTT GATGAGGTAT TATAATTATT TCAATATAAA GCACCCACTA GATGGAGCCA	180
GTGTCTGCTT CACATGTTAA GTCCTTCTT CCATATGTTA GACATTTCT TTGAAGCAAT	240
TTTAGAGTGT AGCTGTTTT CTCAGGTTAA AAATTCTTAG CTAGGATTGG TGAGTTGGGG	300
AAAAGTGAAT TATAAGATAC GAATTGAATT AAGAAAAAGA AAATTCTGTG TTGGAGGTGG	360
TAATGTGGGT GGTGATCTTC ATTAACACTG ANCTAGGGNT TTGGGGTTG GTTTATTGTA	420
GAATCTATAC CCCATTCA NA GAAGATACCG	450

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CTGCAGCCAG TAAACAAGTT TTCATGCAGG TGTCAGTATT TAAGGTACAT CTCAAAGGAT	60
AAGTACAATT GTGTATGTTG GGATGAACAG AGAGAATGGA GCAAGCCAAG ACCCAGGTAA	120
AAGAGAGGAC CTGAATGCCT TCAGTGAACA ATGATAGATA ATCTAGACTT TTAAACTGCA	180
TACTCCTGT ACATTGTTT TTCTTGCTTC AGGTTTTAG AACTCATAGT GACGGGTCTG	240
TTGTTAATCC CAGGTCTAAC CGTTACCTTG ATTCTGCTGA GAATCTGATT TACTGAAAT	300
GTTCCTTCTTG TGCTTATAGA ATGACAATAG AGAACGGCAG GAGCACAACG ACAGACGGAG	360
CCTTGGCCAC CCTGAGCCAT TATCTAATGG ACGACCCAGG GTAACCTCCG GCAGGTGGTG	420
GAGCAAGATG AGGAAGAAGA TGAGGAGCTG ACATTGAAAT ATGGCGGCNA GCATGTGATC	480
ATGCTCNTTG GCCCTGTGAN TC	502

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 499 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CTGCAGTGT	60
CTCTTCTCC	
ACTTAAAACA	
TGAAGTAATA	
ACCCCTCGNT	
CTCTCAACTG	
CTCCTGACCA	120
TCACAGAGGA	
TGGGCTCTCC	
AGCTAAGTCA	
TGCCCCCTCA	
ATGNAGAGGC	
CTTCAAGGTG	180
ATGATGACAT	
GCTGTAAAGA	
AAAGCCACAC	
TGGGTTTGAG	
AATAATAAAA	
CAAAACTCAT	240
ACGTACAGCT	
GCCCCATCCTT	
CCGGGTATAAA	
AAGCTGACTG	
ACTTAATGGT	
AGCCACGACC	300
ACCACCATGC	
AGAGAGTCAC	
AGGGACAAAG	
AGCATGATCA	
CATGCTTGGC	
GNCATATTT	360
AATGTCAGNT	
CCTCATCTTC	
TTCCCTCATCT	
TGNTCCACCA	
CCTGCCGGGA	
GTTACCNNTGG	420
GTCGTCCATT	
AGATAATGGG	
TCAGGGTGGC	
CAAGGCTCCG	
TCTGTCGTTG	
TGCTCCTGCC	480
GTTCTCTATT	
GTCATTCTAT	
AAGCACACAAGA	
AAAACATTN	
CAGTAAATCA	
GATNCTCAGC	499
AGAATCAAG	

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 500 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TAACTCCAG	60
GNTCAAGATN	
TCTNCCTGCG	
TTAGCCTCCT	
GAGTAGCTGG	
GACTATAGGT	
ATGTGCCACT	120
ATTCCCTGAAA	
ACATAATCAG	
TTTGAAAGGT	
AGTGTCTGGG	
CTGGGCGCAG	
TGGNTCACGC	180
CTTCAATCCC	
AGCACTTTGG	
GAGGNCGAGG	
TGGGCGGATC	
ACCTGAGGTC	
AGGAGTTCGA	240
GACCAGCCTG	
ACCAACATGG	
GATAAGACTC	
CATCTCTACT	
AAAAATACAA	
AAAATTAGCC	300
AGGCATGGTG	
GNGCATGCCT	
GTAATCCAG	
CTACTCAGGA	
GGNTGAGGNA	
GGAGAATTGG	360
TTGGAACCTA	
GGAAGCAGAG	
GCTGTGGTGG	
AGCCGAGATC	
GCACCATTGG	
ACTCCAGGCT	420
GGGNAACAAG	
AGTGAACATC	
CNTCTAAAAA	
AAAAAAAAAA	
AAAGGTAGNG	
TTTTGNCCGG	480
NGCGGGGGGT	
CACGCCTGTA	
ATCCCAGNAT	
TGGGGANGGC	
AAGGNGGGGG	
GTCANNANGN	500
NAGNAGTCCG	

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCTGCT GACATGTCCT ATGTTCTTT CTCCCCTACT CCTTCCTACT GTCAGNAATG	60
AAGGGTAGGG CTCCAGCCTG GACCCTGAAG TAAGCTAGAG GTTAAAGCT AAAGAAGAAA	120
GAAGGAGATT GAGTCCTTNG ATGAAACGTGA AGCCACCGTA CTAATCTGGA CTGCCTACCT	180
CTGCACTACT CTATGAGAGA GAAAGTATGT GCATTATTAA ACCAGTTGG GTTGATTTTC	240
TATTAACAAA GTCAGAAACA TCTCTGTAAA AAGCCAGACT GAATATTAA AGCTCTATGG	300
GTCATATGGT CTCCAGGGCA AACACTCAAC TGTGCTACTG TAGTGTGAAA GCAGGCACAG	360
ACAATGTATT AACCAAGGAG GGTGGTCACT TTCCAATGAA AGTTTATCAC AAATTGGNGA	420
ATACTTGGTA TTACACCNNG GGGGAAGGTA GGAGAAGATC TTGCCTGTGG TTGTNGNTGG	480
CAATGTTGGT CTTTTATACG 'NG	502

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 495 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCTCTC CTTAGAAAGTT CCATACACAA CACATCTCCC TAGAAGTCAT TGCCCTTACT	60
TGTTCTCATA GCCATCCTAA ATATAAGGGA GTCAGAAGTA AAGTCTGGNT GGCTGGGAAT	120
ATTGGCACCT GGAATAAAAAA TGTTTTCTG TGAATGAGAA ACAAGGGAA GATGGATATG	180
TGACATTATC TTAAGACAAC TCCAGTTGCA ATTACTCTGC AGATGAGAGG CACTAATTAT	240
AAGCCATATT ACCTTCTTC TGACAACCAC TTGTCAGCCC ACGTGGTTTC TGTGGCAGAA	300
TCTGGTTCTA TAACAAGTTC CTAATAAGCT GTAGCCAAAA AAATTTGATG AGGTATTATA	360
ATTATTTCAA TATAAAGCAC CCACTAGATG GAGCCAGTGT CTGCTTCACA TGTAAAGTCC	420
TTCTTTCCAT ATGTTAGACA TTTCTTGAA GCAATTAG AGTGTAGCTG TTTCTCAGGT	480
TAAAATTCTT AGTAG	495

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

TATGGTTGCC TATTCTGTC ACAGTAACTN AACTGATCTA GGAAAGAAAA AATGTTTGT	60
CTTCTAGAGA TAAGTTAATT TTTAGTTTC TTCCTCCTCA CTGTGGAACA TTCAAAAAAT	120
ACAAAAAGGA AGCCAGGTGC ATGTGTAATG CCAGGCTCAG AGGCTGAGGC AGGAGGATCG	180
CTTGGGCCCA GGAGTTCACA AGCAGCTTGG GCAACGTAGC AAGACCCCTGC CTCTATTAAA	240
GAAAACAAAA AACAAATATT GGAAGTATT TATATGCATG GAATCTATAT GTCATGAAAA	300
AATTAGTGTA AAATATATAT ATTATGATTA GTTATCAAGA TTTAGTGATA ATTTATGTTA	360
TTTGGGATT TCAATGCCCTT TTTAGGCCAT TGTCTCAAAA AAATAAAAGC AGGAAAACAA	420
AAAAAGTTGT AACTTGAAAA ATAAACATT CCATATTTAT AGCCAACCTAA GTGGGTTTNG	480
GGTNGGTTGG GTTGGTTGGT	500

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTATCATTAA CAGGTCCAC AACCCTTAAA AAGTACAGAT TTTTTTTTTC TTNGTGGAGA	60
CAGGGTCTCA CTTGGTCGCC CAGACTGGAG TGCAGTGGCA CGATCTCAGT TCACCACAAAC	120
CTCTGCCTCC TGGGTTCAAG CAATNCTCGT GCTTAAGCCT CCTGAGTAGG TGGAACCACG	180
CGTGCACGCC ACCACCGCTAG GTTNATTGTG GCTTTTTAG TAGAGACAGG GTTTCGCCAT	240
GTTGCCAGG CTGGTCTCAN ATTCCNGACC TCAAGTGATC CGNCCGCCTC AGACTCCCAA	300
AGTGNTGAGC ATTACAGNTG TGTACCACTA TGTCCNGNC CNCATCTCTC TTTAAAACAN	360
CTTNCATTTA CCTAGTCCAC TCCTG	385

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GACCTAGAAA AGAAAGCATT TCAANNTAAT TAACAGGTCC CACAACCCTT AAAAAGTACA	60
GATTTTTTTT TTCTTNNGG AGACAGGGTC TCACCTTGTC GCCCAGACTG GAGTGCAGTG	120
GCACGATCTC AGCTCACCAAC ANCCTCTGCC TCCTGGGTTA AAGNANTTCT CGTGCTTANG	180
CCTCCTGAGT AGGTGGAACC ACGCGTGTGC GCCACCACGC TAGGCTACTT TNTGTATTT	240
TAGTAGAGAC AGGGTTTCGC CATNTTGCCC AGGCTGNTCT CAAATTCCCTG ACCCNCAAGT	300
GATCCCCCN CCTTCAGTAC TCCCCATCAG	330

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GGTGGNCGTT CTAGAACTAG TGGCNCCCAA GGNAGAAGAA GTTTCTTAG TACAGAACAA	60
AATGAAANGT CTCCCATGTC TACTTCTTTC TACACAGACA CGGCATCCAT CCGTTTTCT	120
CANTCTTCC NCCACCTTTC CCGTCTTCT ATTCCACAAA GCCGNCATTG TCATCCTGGC	180
CCNTTCTCAA TGAGCTGTTG NNTACACCTC CCAGACGGCG TGGTGGNCGG TCAGAGGGC	240
TCCTCACTTC CCAGTAGGGG TGGCCNGCA GGNGGTGCC CNCACCCCCC GGGCGGGGTG	300
GTTNGTCCNN CCGGNGGGNT GCACCNCACC CACCCCTCCC CNCTCTNCTA CTGGCGGTG	360
TNTATTNCAN NATTTAAG CA	382

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GGATCCAAAG GAAGTTAGAG GCCAGCTCAG TCTACACCTG CTACTGNTCA GTGCCACCC	60
GGTCAAGGGA GACCAACACA TGGTAAAGGT CAAGGGCTTC TTGGAAGGCA GTCAGCAGCC	120
TGTGCAAGAT GTTCTCCACA CTGCTCAGNT TAAGGGGAGC TGGGGGCAGG ACCTCAGCTG	180
GNATCTCTGC TTCACCAAGTG TCCAGGGTT GCACAATTCT TGTTTACTCG TAGGATATTT	240
AATCTTGGNN GGTGCTATCA TAAATGGGAC TTATCCNCTN ATTATGTTTT CTTACTAGTT	300

GTTTATGTGA AGGTTATTGA TTTGGGTTTC ACTTTATTTN GTGGNAATGG AGTTCACTC 360

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AATGTCACGG ATTCCCTTAG GTAGNTACAC CCATCAACCT TTTTGAGAAT AAAATGAATT	60
GAGAGTGTAA CAGTCTAATT CTATATCACA TGTAACCTTT ATTTGGATAT ATCAGTAATA	120
GTGCTTTTTT TTTTTTTTTT TTTTTTTTNG GNGANAGAGT CTCGCTCTGT	180
CGCCAGGTTG GAGTGNAATG GTGCGATC	208

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 470 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

AACAAGGTTT CTCGGTCGGC GGTGAATATA CCGGGCGTC GATATTGTT GCGGAATACT	60
CCCTGACCG TAAACGTGGC TTTATGGCA GCTGGCTGGA CTTCGGTTCT ATTGCCGGGT	120
TTGTGCTGGG TCGGGCGTG GTGGTGTAA TTTCGACCAT TGTCGGCGAA GCGAACTTCC	180
TCGATTGGGG CTGGCGTATT CCGTTCTTA TCGCTCTGCC GTTAGGGATT ATCGGGCTTT	240
ACCTGCGCCA TCGCCTGGAA GAGACTCCGG CGTTCCAGCA GNATGTCGAT AAACCTGGAAC	300
AGGGCGACCG TGAAGGTTTG GAGGATGGCC CGAAAGTCTC GTTTAAAGAG ATTGGCACTA	360
AATACTGGNG CAGNCTGTTG AATGTTGGG CTTGTAATT GGCAACCAAC GTGATTACTA	420
NATGTTGGTG ACCTATATTG CCGAGTTATT GGCGGATAAC CTGAATTATC	470

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TAATTATATT GAAATGCTTC TCNTCTAGGT CATCCATGNC TGGNTTATTA TATCATCTCT	60
ATTGNTGNTG CTCTTTTTA CATNCATTAA CTTGGGGTAA GTTGTGAAAT TTGGGGTCTG	120
TCTTCAGAA TTAACTACCT NNGTGCTGTG TAGCTATCAT TTAAAGCCAT GTACTTTGNT	180
GATGAATTAC TCTGAAGTAA TAATTGTNTC CACATATAGG TCATACTTGG TATATAAAAG	240
ACTAGNCAGT ATTACTAATT GAGACATTCT TCTGTNGCTC CTNGCTTATA ATAAGTAGAA	300
CTGAAAGNAA CTTAAGACTA CAGTTAATTCA TAAGCCTTTG GGGAAGGATT ATATAGCCTT	360
CTAGTAGGAA GTCTTGTGCN ATCAGAATGT TTNTAAAGAA AGGGTNTCAA GGAATNGTAT	420
AAANACCAAA AATAATTGAT	440

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

AAAACAAAGC CTCTTGAGGT TCTGAAAAGG GAAAGAAAAA CAGAACTTTG TGCAC TACAA	60
TTATACTGTT ATAAAAAAACA CTTCCATAGA TTACATTAAG CAGAAACAAA CCTTTCTTTC	120
ATGTGTTCTC CTCCAGGCCA AGCTGTCTAA GGACCGCAAA GGCTGTTGTC ACTTGCAGGC	180
TCCCAGATTA GGTCTGAAAT AGGATTTCAC CAGGTCA TCC ATTGTTAGTT AAATCCTAGT	240
AAATTCA TTT ANACCAATCA AATACTTATA AGACCAATTT GTAAACCAGG AATGTATTAA	300
TTTGTCA CGA CTTTCAACTA ACTGACAAAT TTACTATAAG CTCAGGTAG GACTCTTTAG	360
CAATAAGTAG GAACCGCCTG AGACAACCAA ACATTTCAA CCCACAAANG ATACTTTAAT	420
GACTTTCTGA TTTNCCAGCA AAAGGGGGG	449

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 425 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGATCCGCC CTCCTCGGCCT CCCAAAGTGT TGGGATTACA GGCGTGAGCC ACCGCACCTG	60
GCTTTTTTTT TTTTTTTTTT TGGNGGAGAC AGAGTCTTAC TCTGTTGCCA AAGCTGGAGT	120
GCAGTGGTGC AATCTTGGTT CACTGNAACC TCCACCTCCA GAGTTCAAGC AATTCTCTGC	180
CTCAGTTCT GGAGTAGCTG GGATTACAGG TGCCTGCCAT CACGCCTGGC TAAATTTGGN	240

ATTTTTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGGTCTT GAACTCCTGA	300
CCTTGTGATC CACCAGCCTC GGCCTCCCAA ATTGNTGGGA TTACAGGCCT GAGCCACCAC	360
AACCAGGCTA AAGTTTAAA ACATGCCAAG TGTATTTACA TAATGCGATA CGANTTATGT	420
ACATA	425

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 386 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGATCCGCC GCCTTGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNTTGTAA AATAAGCATG TTATCTGTCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTGG GCCAGCATAG AAAAAGGAAT	300
GTTGAGAACCA TTCCNTTAAG GATTACTCAA GCTCCCTTG GTGTATATCA GNNGTCANNA	360
CNTATCTTNG GGGCTGAAAA ATGTTT	386

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAAAAGGGAA AGAAAAACAG AACTTTGTGC ACTACAATTA TACTGTTATA AAAAACACTT	60
CCATAGATTA CATTAAGCAG AAACAAACCT TTCTTTCATG TGTCTCCTC CAGGCCAAGC	120
TGTCTAAGGA CCGCAAAGGC TGTGTCACT TGCAGGCTCC CAGATTAGGT CTGAAATAGG	180
ATTTCACCAAG GTCATCCATT GTTAGTTAAA TCCTAGTAAA TNCA	224

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GGATCCGCC	TCCTCGGC	CCC	AAAGTGT	TGGGATTACA	GGCGTGAGCC	ACCGCAC	CTG	60
GCTTTTTT	TTTTTTTT	TGG	NGGAGAC	AGAGTCTTAC	TCTGTTGCC	AAGCTGGAGT		120
GCAGTGGTGC	AATCTGGTT	CA	TGCAACC	TCCACCTCCA	GAGTTCAAGC	AATTCTCTGC		180
CTCAGTTCT	GGAGTAGCTG	GGATTACAGG	TGCCTGCCAT	CACGCCTGGN	TAAATTGGG		240	
ATTTTTTT	AGTAGAGACA	GGGTTTCANC	ATGTTGCCA	GGNTGGTCTT	GGACTCCTGA		300	
CCTGGTGAAC	CACCAGGCTC	GGGCTCCAAA	TTGGTTGGG	ATTACAGGGG	GTNAANCAAC		360	
CACAACCCAG	NCTAAAGTTT	TNAAAACATN	CAAAGTGT	TTT	AAAATNATG	NGATACGATT		420
TATTGTACAA	TTAATT	TTAT						440

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GTCTTCCC	A	TCTCCAC	AGAGTTGT	CCTTACATTA	TTACTCCTTG	CCATTTCAA	60	
GAAAGCATTG	TCAGCTCTTC	CAATCTCCAT	CAC	TTGGG	CTTGT	TTCT	ACTTGCCAC	120
AGATTATCTT	GTACAGCCTT	TTATGGACCA	ATTAGCATT	CATCAATT	TTT	ATATCTAGCA		180
TATTTGCGGN	TAGAATCCC	GGATGTTTC	TTCTTGACT	ATAACAAAT	CTGGGGAGGA		240	
CAAAGGTGAT	TTTCCTGTGT	CCACATCTAA	CAAAGTCAAG	ATCCCCGGCT	GGACT	TTTGG		300
AGGTTCC	CAA	GTCTTCC	TGACCAC	TTT	GCAC	TATTGG	ACTTTGGNAA	360
ATAGAAAACG	ATTTGGAAC	ATACTTCATC	GCAGGGGGAC	TGTGT	CCCCC	GGTGGCAGAA		420
NCTACCAAGA	TTTGGGGNC	GAGGTCAA						448

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGATCCGCC	GCCTGGC	CCC	AAAGTGC	TGGGATTACA	GGCATGAGCC	ACCGCTCCTG	60
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GCTGAGTCTG CGATTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTTNAGTAA AATAAGNATG TTATCTGNCC GCCCTGCCTN	180
GGNNATTGNG ATAAGGAT	198

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CTGCAGTGAG CCGTGATTGC ACCACTTAC TCCAGCCTGG GCAACAAAAT GAGACCCTGG	60
CTCAAAAACA AAAACAAAAA CAAAAAAAGA GTAAATTAAT TTAAAGGGAA GTATTAAATA	120
AATAATAGCA CAGTTGATAT AGGTTATGGT AAAATTATAA AGGTGGATA TTAATATCTA	180
ATGTTGGGA GCCATCACAT TATTCTAAAT AATGTNTTGG TGAAAATTAT TGTACATCTT	240
TTAAAATCTG TGTAATTTTT TTTCAGGGAA GTGTTAAAA CCTATAACGT TGCTGTGGAC	300
TACATTACTG TTGCACTCCT GATCTGGAAT TTTGGGTGTG GTGGGAATGA TTTCCATTCA	360
CTGGAAAGGT CCACTTCGAC TCCAGCAGGC ATATCTCATT ATGATTAGTG CCTCATGGNC	420
CTGGTGTGTTA TCAAAGTACC TCCCTGAATG GACTGCGTGG GTCATCTTGG NTGTGATTCA	480
GTATATGGTA AAACCCAAGA	500

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CTGCAGCCTT GACCTCCTGG GATCAATCGA TCCTCCCACC TCAGCCTCCT AAGTAGCTGG	60
AACTACAGGT GTGCACCAACC ATGCCCGGCT AATNGNTGTA TTTTCTGTAG ATACGAGGTN	120
TNGCCATGTT GCCCAGGCTG GTCTTGAAC TCTGGCTTAG GTGATCTGCC CGCCTCAGCC	180
TCCCAAAGTG CTAAGATTAC AGGCATGAGC TACCATGCC AGCCGAAATC TTCAAATGAA	240
AAAGTTACTA TAGCTAATTA ATGATTTACT GAAGAGTTAT GGGATGTACA CGTTACCATT	300
TTCTCTAAAT CAAGATAAAG AGATGAGGAA AGAAAACACT CCAGTGGGGC ATTCTGTNA	360
CAAAACAAAT TATCAGTCTT GGGGTTTNAC CATATACTGA AATCACAGGC AAGATGAGCC	420

ACGCAGTCCA TNCAGGGAGG TACTGGATAA CACCAGGGNC ATGAGGGACT AATCATAATG 480
AGATATGCTG CTGGAGTCGA 500

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CTGCAGGATG AGAGCGATCT CTTNTTNCAT TTCTCGCT ACGCGCTGCG GGCGACCAAA 60
TTCTTCGCC ATAATAAATT CTCCTGACNA AAAAGGGGCT GTTAGCCCCT TTTTAAAATT 120
AATTCAGGT GGAAGGGCTG TTCACGTTGA CCTGATAAGA CGCGCCAGCG TCACATCAGG 180
CAATCCATGC CGGATGCAGC GTAAACGCCT TATCCCGCAT GGAACCCCTAA AAACCTTAAG 240
CAATGGTACG TTGGATCTCG ATGATTCGA ATACTTCGAT CACATCGNCA GTGCGGACGT 300
CGTTGTAGTT CTTAACGCCG ATACCACATT CCATACCGTT ACGGGACTTC GTTAACGTCA 360
TCTTGGAAAG CGGGGCAGGG ACTCCAGCTC GNCTTCGTAG ATAACCACGT TGGCACGCAG 420
GAACGCGGGT CGGGTTGTGA CGTTAACAC AACTTCCGGG TAACCATAACA GGCTGNGATG 480
GNACCAAATT TCGGGGGATT TGGACAAGTC AAGAACTTCC CGCCAGACCG ATAATCTTGT 540
TGTTCAAGTTC 550

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 541 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA 60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTA 120
TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTCACCT GCCATTTATT TCATATTCA 180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAC CTTTTTCCT TCGTTAAC 240
CTCCCTACCA CCCATTTACA AGTTAGCCC ATACATTTA TTAGATGTCT TTTATGTTT 300
TCTTTNCTA GATTTAGTGG CTGNGTTGTG TCCGAAAGGT CCACTTCGTA TTGCTGGTTG 360
AAACAGCTCA GGAGAGAAAT GAAACGCTTT TTCCAGCTCT CATTACTCC TGTAAGTATT 420

TGGAGAATGA TATTGAATTA GTAATCAGNG TAGAATTTAT CGGGAACTTG AAGANATGTN	480
ACTATGGCAA TTTCANGGNA CTTGTCTCAT CTTAAATGAN AGNATCCCTG GACTCCTGNA	540
G	541

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

NNCCCNCCNN NNNNNNNNTN NTNTGCCCC ATAACATAG GGNGACTTGG AGATCCACCG	60
CGGTGGCGGN CGNTCTAGAA CTAGTGGATC CCCCCGGGNTG CAGGACCCAA CGCTGCCCGA	120
GATGCGCCGC GTGCGGTTGC TGGAGATGGC GGACCGCGATG GATATGTTCT GCCAAGGGTT	180
GGTTTGCAGCA TTCACAGTTC TCCGCAAGAA TTGATTGGCT CCAATTCTTG GAGTGGTGAA	240
T	241

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CCCCCCCNCN NNNNNNTTTN NGCAGCCCCGT AATTACCCCTC ACTNCCGGGA ACAAAAGCTG	60
GGTACCGGGC CCCCCCTCGA GGTGACGGT ATCGATAAGC TTGATATCGA ATTCTGCAG	120
TGTTTAAAAA ATAAAATAAA CTAAAAGTTT ATTTATGAGG AGTACACTGC TTTCTTGAA	180
ACACATGTAC AAGCCATATA ATAGAGTTCA TTTTTTACCC TAGTTACCGA AACACTAGAA	240
AGTCTTCACC CGGCCAAGAT AACACATCTT TAGTAAAAAT AGCAAGAAAT ATTTTATGGG	300
TTGTTTACTT AAATCATAGT TTTCAGGTTG GGCACAGTGG NTCATGCCTG TAATCCCAGC	360
ACTTTATGCG GNTGAGGCAG GCAGATCAGT TGAGGTCAGA AGTTGGAGA CCAGNCTGGG	420
CAATGTGGNA AAACCTCATC TCCACTAAA ATACAAAAT TAGNCAGGCA TGGTGGTGCA	480
CACATGTAAT TCCAGNTACT TGGGGAGGCT GAGACAGGAG GATCGNTTGA ACCTAGGGAG	540
GGAGGGAGTTG GAGTGAGCTA ATGTCAATGC ACTCTTGGTT GGGGCGANAG AGCAAGATCT	600
TTCTTCCAAA AAAAAAAA AAAAAAAAGC CAGGTGNGGN GGTCAAGGCT GTAATCCAGA	660

ATTNGGGAGG CCGNGGAGGN NATCANTGNG GNAGGGNTCA AGNGGGCNG GCCACATGGG	720
GAACCCGTTN TTNTTAAATN AAAATTAGCC GGGGNGGGGG AGGACTNTAT CCNGTTCCGG	780
NGGTGNGGAG GATCNTTATT NTGGNGGAGG GTGGATGNNC CAGTTGACNC CCCC	834

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTGGGCNCNC GCCCCTTAAN TTTTATNGN TTNCTANAAA AANANNNGC NCNNTAAAAT	60
ATATTTTTTN TTGTGACCCC TTTAAAAGG GACCCNCTAA AAAATTTNT GGTTNNNTTN	120
GATTTANGTG GGTGNTTTN TTATATTTT GGNGAGNNTC TGTAGTCNTC NCCCTCAAAC	180
ANNTCNTACN ATNGGNANCG TGACTCTGTC NTTNGTNANN NTCGNTNTCN NGTNATTCA	240
GGNNCCTCGC GCNNCNCGGG CNNNGTTTT TTTNNCNNT TTTAAGCCNA ANNCTCAGTA	300
NCNTCCAACG GNGCTNNGAC ANNNNGNNCT NTCGNGGGTN CCCTCTNTNT NGNNCNGGC	360
TNNNGNNNNC NGNCNCNGN GCCNTGCGNN NNGNNNGGG NNNGNTNNCA TANGGATNGN	420
GNTGCTCNNC NCNNNGTNNA TNAGTAGGNA NTTTNTNNNT ACTTGCCNNC NNNTNGCTGC	480
GAGNANAGCN ANNTNGNNGN AGNGNNNGNTG CGCGGANNTT CCCCTGATNA NCTCGAGCNG	540
NTTACNGGNG CNNCCTNGAA NAAGNGNNGT ANNGTGCCGA GNCGCTANN NC TGAGCCTGAG	600
TNTCGACNGG NATNGTGNNT CNTACNGTTA NGGGNNGCNN GANCGGGNTG ANTNCNGGN	660
NGANCNAGCG ACTGCCTNTC ANGCGAANCG TNTCANGNNN GTAGAGCANA GGGTNANNNG	720
TCNNNNAAAGC NTNNAGTGAN TGTCTNACN NGTGANNTAC GGCNTAGNCT TGATNTNNAN	780
NCGAGGNNNN ATNNANNNTT GGANANTNN TNNNNTCNCN TCGCGNGNG NCNNNGCCG	838

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 803 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATTCGCGCGT AGCCCGATAA CTATAGGGCG ACNTGGAGNT CCACCGCGGT GGCGGCCGCT	60
CTAGNAACTA GTGGATCCCC CGGGCTGCAG GAATTACACGG ACTAATCCTC TACAGATCTT	120
GCTGGAGTGG CCTTCAGCC TTTTGTGACT GTTTGTAGTG AAATGTACAC ACAAGCCTAC	180

AAGGCAGCCC AGATGTACCA TAACTGTGGG AAAATTAAAA AAAAAAAAAC ACAGAACCTC	240
TCTATGTTGC CCATGCTGGA CTCAAACTCT TAGACAAGCA ATCCTCGTAC CTCAGCCTCC	300
TGAGTTCTG AGTAGCTGGG ACTACAAGCA TGCACCACCA TGCCAGGCTA TGAGAAAGTT	360
CTTTTATTG ATCCAGACCT TATTGCCTGG TAACTTCCAC CACTGTTCCCT AGCTCTGNTC	420
TCTGGTCCTA ACAGAGGAAA ATCTTGACCC CACACCTAGT GCAACTGGAT AGCTTATNGT	480
TGGGCTNGT TTTCCTCTAT TCTGGTCCA CCCTAAAATC CNATAGATAC TCCAAGTGCT	540
CANAGNAAC CAAGCTCTCT CTCTNNCTTN CTTTCTTNNN CTCTATTNAT TNATGGGNNA	600
TNATTNATTN NGGGGATGGN GTTCGGTCGC CGCCCGGCTG GNGTGAATG GGGGAGGCAA	660
TCAATTTAAC CCCACCCNGG GTCCAGGGAT CTCGTTNAAA CCGNNNNNNN NNNNNNNNNNA	720
NGNNCCNNCNC NNNCCNNTNN NNNGTTTN NNNGNNNGG NNNCCNNNN NANNNNNNNTN	780
NNNCCNCCNA NNNTNCNNNN CCC	803

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 780 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

CNNNNNNNCC CNNTNATTNT ACGCCAGCCG CGTAATTAAC CCTCACTAAA GGGAACAAAA	60
GCTGGGTACC GGGCCCCCCC TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCCA	120
ACTCCTCACT TGCCAGATGT GACCTTAAGC AAGTGAACCTT CTGTGTGCCA CACTGTTTC	180
ATCTGTAAAA GGATAAAAGGG AATATCATAA ATTAGTTGT TAAGCCTTAG TTTAATAATG	240
TCTCTAAGTT TTACATATAA GTAGACAGTG TCTTCTTGT TTAGTGAATA ATCATTCTTA	300
TTATTTAATA GTATCTCTAC TAAATTTATT GTGTAAGATT ATACTAATCT TGTTTAGTGC	360
GTGGTAATCA CTTCTGCTCA TATTTAACCT ATAAGCATAA TATAGTTTAT TTATATACCA	420
NTTATTTATT TTATTTTATT TGNNGAGATG CAGCTTGTCT TTTNCAACCC AGGGNTGNNG	480
NGNAGNNGNG NAANCTTGNT TCACTGNAAC CNCCACCNCC CAGGTNCAAG NGATTCTCCT	540
GNTCAAGCCN CCTNAGNAGN TGGNATTACA GNACGANTAC ANNCCAGNTA NNNNGNTNT	600
NNGNTNGNN NAANCTTGNT TCACTGNAAC CNCCACCNCC CAGGTNCAAG NGATTCTCCT	660
CCCCNNNGNN NNNNATANAG NATNANCANN NNCCNCNNNN NCNNNNNNNG GNGGANCCN	720
NNTNGCNGNN ANNGNNANNN NNTNNNNNNN NNGNCNNNG NNNNNNNNCC NNNNNNCCCC	780

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 803 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

NNNNNNNNNC	CNNNNNNNTTC	GNNCGTAACN	CGANTCACTA	TAGGGCGACT	TGGAGCTCCA	60
CCGCGGTGGC	GGCCGCTCTA	GAACTAGTGG	ATCCCCGGG	CTGCAGGAAT	TCGATATCAA	120
GCTTTNGTGT	GTAAAAAGTA	TTAGAATCTC	ATGTTTTGA	ACAAGGTTGG	CAGTGGGTTG	180
GGAGGAGGGA	TTGGAGATTG	ATGCGATAGG	AATGTGAAGG	GATAGCTTGG	GGTGGATTTT	240
ATTTTTAAT	TTTAATTTT	ATTTNTTGAG	ATGGAGTCTT	GCTCTGTCTC	CCAGGCTGGA	300
GTGCAGTGGT	GTGATCTCAG	CTCACGGTT	CAAGCGATTC	TCCTGCTGCA	GCCTCCGAG	360
TAGCTGGGAT	TACAGGAGCG	CGCCACCACA	CCCGGNTAAT	TTNNNTGTAT	TTTTAGTAGA	420
GACGGGGTTT	CACCATGTTG	GTTAGGCTGG	TCTAGAACTC	CCAACCTCAT	GATCCGCCTG	480
CTTCGGCCTC	CCAAAGTGCC	GGAATTACAG	GCGTGAGCGA	CTGCACCCGG	CCGCTTGGGG	540
GTGGATTTT	AAAGAAATTT	AGAAGAATGT	AACTTGGCCA	GATACCATGT	ACCCGTTAAT	600
TCATTTNCGG	TTTTTGGAT	ACCCATTTG	NNATTCTCCC	NCCACTGGAT	AAATAAGGGN	660
GGTCATTNT	NGNTTAGTTT	GGGTNTTTT	NAGTGTGGNT	TCTGCTTATN	ATTAGAATGG	720
NCTNCTTNC	CAANCTGGAA	AGGGAGGAGT	AAAATCANT	ACCAAGANCA	GAAATTCTTT	780
TCANTTGTG	CNCNAGAAAT	GCC				803

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 819 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TNCCNNNNCN	NNNNNAATTT	TNGCAGNCGC	GTAATTAACC	TCACTAAAGG	GAACAAAAGC	60
TGGGTACCGG	GCCCCCCCCTC	GAGGTCGACG	GTATCGATAA	GCTTCCCTCC	CCTTCCTCAG	120
CTCTGGCGAC	CCTGCGCTGT	GGTGGTTCTC	CAACCCACACT	CATTCTCCTC	AGCTGGCTCC	180
TTGCTCTTCT	TCCACCCCT	CGTTGGAAGT	GTTCTTAAGT	GTTCGGCTTG	GCCTCCTCTT	240
CCCCTTCCTT	AGNTTAGACT	TCTCCACTGC	TCCAACATCA	ACTGGAAATC	TATGGAATTG	300
ATTCCTGTTT	TCAGCTCCAG	TCCTGTTCAC	AGGGCATT	CACCTGCTGG	CACTTCCAAA	360
GTGACACTTC	CAAACCACTT	CCTCGCCCTC	CTCTCTAAC	CAGGTCTTTC	TTCTAACTT	420

CCTTATTCCT GAGAATGTCT CTGNCATGTT	CTAAACTGAA AACTCCTAGT CAACTNCACA	480
CTTTATTCCC TGGATCCTCA ATTGGGTTCC	CATGTNCCGT TAGTGTTCCT TGGTAAGNCT	540
CTGCCANCAC CGNAGGATCG ACTCTAATCA	CATCTCAACT GAATTATGGN AAAGTCAACT	600
CAATTCTCTC AACCATCCCA GGCTCCACTA	TGGNTAATAT GCTAAGGAGA GCTGACCCAA	660
CGGGGAGAAG ATCTGNGGG GAGGAGAGAA	ACAAAGNTAA TGGAATNATT CTCGAAAAGC	720
CCACAAGGNG AAGGATAACC CNCTTCCNCT	CGAAAGAGGG GGGATGCCA GATNTCGCGC	780
CCGGAAAGAA ACCGGGNGA GGGGTTACA	NTGTAAGNC	819

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 796 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

TNTTGGCTGG TACTGCTTGA	GCAACTGGTG AAACCTCCGCG	CCTCACGCC CGGGTGTGTC	60
CTTGTCCAGG GGCGACGAGC	ATTCTGGGCG AAGTCCGCAC	GCCTCTTGT CGAGGCGGAA	120
GACGGGGTCT GATGCTTTCT	CCTTGGTCGG GACTGTCTCG	AGGCATGCAT GTCCAGTGAC	180
TCTTGTGTTT GCTGCTGCTT	CCCTCTCAGA TTCTTCTCAC	CGTTGTGGTC AGCTCTGCTT	240
TAGGCATATT AATCCATAGT	GGAGGCTGGG ATGGGTGAGA	GAATTGAGGT GACTTTCCA	300
TAATTCAAGGT GAGATGTGAT	TAGAGTTCGA TCTGCGTGG	TGGCAGAGGC TTACAAGAAA	360
CACTAACGGG ACATGGGAAC	CAATTGAGGA TCAGGGAATA	AAGTGTGAAG TTGACTAGGA	420
GGTTTTCACT TTAGAACATG	GCAGAGACAT TCTCAGAAAT	AAGGAAGTTA GGAAGAAAGA	480
CTGGTTTACA GAGGAGGGCG	ANGAAGTGGT TTGGGAAGTG	TCACTTGGG AAGTGCCAGC	540
AGGTGAAAAT GCCTGTGACA	GGATGGAGCT GAAAACAGGA	TCAATTCCAT AGATTCCAGT	600
TGATGTNGGA GCAGGGGAGA	AGTCTTAGCT AAGGAAGGGG	AAGAGGAGGC CAAGGNAACA	660
CTTAGGACAA TTGNAACGAN	GGGGGGGGAG AAGAGNAAGG	GCCACTTAGG GGAATAATNT	720
GGTGGGGGAC CCCAAGNNA	GGCGCANNN TTAGGAGGGG	GGGANNTCAN AGGAAAGTGG	780
AAGNTTGGGT TTANCT			796

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTCGTCGTA NCCCGATNAC TATAGGGCGA CTTGGAGCTC CACCGCGGTG GCGGNCGC GG	60
GCAGGGNCCG GNCCCTTGTG GCCGCCGGG CCGCGAAGCC GGTGTCTAA AAGATGAGGG	120
GCGGGCGCG GNCGGTTGGG GCTGGGAAC CCCGTGTGGG AAACCAGGAG GGGCGGCCG	180
TTTCTCGGGC TTCGGCGCG GCCGGGTGGA GAGAGATTCC GGGGAGCCTT GGTCCGGAAA	240
TGCTGTTGC TCGAAGACGT CTCAGGGCGC AGGTGCCTG GGCGGGGATT AGTAGCCGTC	300
TGAACGGAG TGGAGTAGGA GAAAGAGGAA GCGTCTTGGG CTGGGTCTGC TTGAGCAACT	360
GGTGAAACTC CGCGCCTCAC GCCCCGGGTG TGTCCTTGTG CAGGGCGAC GAGCATTCTG	420
GGCGAAGTCC GCACGCCTCT TGTCGAGGC GGAAGACGGG GTCTTGATGC TTTCTCCTG	480
GGTCGGGGAC TGTCTCGAGG CATGCATGTC CAGTGACTCT TGTGTTGGT GNTGCTTCCC	540
TCTCAGATCT TCTCACCGNG GTGGGCAACT CTGTTAGGC ATATTATCCA TAGNGGAGGC	600
TGGATGGTTG AAANAATTGA GGTNATTTC CATAATCAAG TGAAATTGAGA TAGAGTCCGN	660
CTTTNGGGGT GNAAGGGTTA AAAAAAAATA ACGGAAATGG AACAAATGAGG TCAAGGATTA	720
GTGAGTTGN TAGNGGTTCA ATTAGANATG AAGGNATCTA AAATAGGAGT AGAGAANNNG	780
TTNAAAGAGG GAAAATTTG CC	802

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

ATATGCAGCC GCGTAATTAA CCTCACTAAA GGGAAACAAAA GCTGGGTACC GGGCCCCCCC	60
TCGAGGTCGA CGGTATCGAT AAGCTTGATA TCGAATTCT GCAGCCCGGG GGATCCGCC	120
CGCGGCCTCC CAAAGTGCTG GGATTACAGG CGTGAGCCAC CGCCCCGGGN CTCACATTT	180
ATTTCTATTG GCTAGCGCTG CTCTAAATCT TCTGTTCTT CTGCTACACC AGGCCTAAC	240
CTCAAAATCC CTGCCAACCT TTCCCTTCCT GAAGCTTCCC TCCCCCTCCT CAGCTCTGGC	300
GACCCTGCGC TGTGGTGGTT CTCCAACCAC ACTCATTCTC CTCAGCTGGC TCCTTGCTCT	360
TCTTCCACCC CCTCGNTGGA AGTGTTCCTA AGTGTGGC TTGGCCTCCT CTTCCCTTC	420
CTTAGCTTAG ACTTCTCCAC TGCTCCAACA TCAACTGGAA ATCTATGGAA TTGATTCTG	480
TTTCAGCTCC AGTCCTGTT ACAGGGGATT TTCANCTGGT GGCATTTCCA AAGTGAATT	540
CCAAACCACT TCCTCGGCCT CCTCTTCTAA ANCAGGTCTT TCTTCCTAAC TTCCTTATTC	600
TTGAGAATGT CTCTGCATGT TCTTAAANTG AAAACTCCTA GTCAAATTCA AATTATCCC	660

TGATCCAAA TGGTCCCATT CCCGTAGGGT TTNTGTAGCC TGCACACCGA GGTGGANTT	720
TATNNATTCA CCGATTATGG AAAGTAACCA ATCTTNACCA NCCAGCTCAT TTGTTNTNTG	780
CTAAGAGGGT NCC	793

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

AAAGTCATGG ATTCCCTTAG GTAGCTACAT TATCAACCTT TTTGAGAATA AAATGAATTG	60
AGAGTGTAC AGTCTAATTC TATATCACAT GTAACTTTA TTTGGATATA TCAGTAATAG	120
TGCTTTTCN TTTTTTTTT TTNTTTTTT TNNTTTNGG GGANAGAGTC TCGCTCTGTC	180
GCCAGGTTGG AGTGCAATGG TCGCATCTTG GCTCACTGAA AGCTCCACCN CCCGGGTTCA	240
AGTGATTCTC CTGCCTCAGC CNCCCAAGTA GNTGGACTA CAGGGTGCG CCACCACGCC	300
TGGGATAATT TTGGGNTTT TAGTAGAGAT GGCGTTTCAC CANCTGGNG CAGGCTGGTC	360
TTGGAACCTCC TGANATCATG ATCTGCCTGC CTTAGCCTCC CCAAAGTGCT GGGATTNCAG	420
GGGTGAGCCA CTGTTCCCTGG	440

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTTAGTCTGT NTCGTAGTCA TATTAATTGT AAGTNTACAC TAATAAGAAT GTGTCAGAGC	60
TCTTAATGTC AAAACTTGAA TTACACAGTC CCTTTAAGGC AGTTCTGTT TAACCCCAGG	120
TGGGTTAAAT ATTCCAGCTA TCTGAGGAGC TTTTNGATAA TTGGACCTCA CCTTAGTAGT	180
TCTCTACCCCT GGCCACACAT TAGAATCACT TGGGAGCTTT TAAAAGTGTA AGCTCTGCC	240
TGAGATATTC TTACTCAATT TAATTGTGTA GTTTTAAAAA TTCCCCAGGA AATTCTGGTA	300
TTTCTGTTA GGAACCGCTG CCTCAAGCCT AGCAGNACAG ATATGTAGGA AATTAGCTCT	360
GTAAGGTTGG TCTTACAGGG GATAAACAGA TCCTTCCTTA GNCCCTGGGA CTTAATCACT	420
GAGAGTTGG GTGGNGGTTT NGNATTTAAT GAC	453

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 369 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GACACACATT CACACATAAT TATGAAAGCA TTTTCAGGCA AAACTCAATC ACAAGTCTGG	60
GTTTTAACCA TAGTTAACTG AATATTTCCC TTGGGGGGTT AAATTTAGA ACAGACGTNC	120
ATNCAATCTG GAAGAAGAGC TATGAAAAAA ACCTAGCTTG GGTNGGTTTC ATAGGGTNCA	180
TTATGNACAC ATTGTTATTT TATCCCTTAA TNCTAGTAAA GAAATAGAAT CTGAAAATAA	240
GTAAAACATAC TTGGAAAAAA NTTAAAAGAT ACAGAAATTT CTATCTTAAA TGATGTGTGG	300
GCCNCTGTGA TTTTAGTNGG GNTGGTTAAA ANCCCAGAGG TGAAGAGNAT NCTCTATGCT	360
GTGNGGGGG	369

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GCTCATCATG CTTCACGGGG GAGGCTGTGC GGGAAAGAATG CTCCCACACA GNATAAAGAA	60
TGCTCCCGCA CAGGATAGAG AATGCCCG CACAGCATAG AGAAGCCCCC GCACAGCATA	120
GAGAATGCC CCNCACAGCA TAGAGAAGCC CCCGCACAGC ATAGAGAATG CTCTTCACCT	180
CTGGGTTTTT AACCAAGCAA ACTAAAATCA CAGAGGSCMA CACATCATT AAGATAGAAA	240
TTTCTGTATC TTTAATTY TTTCMAAGTA GTTTTACTTA TTTTCAGATT CTATTTCTTT	300
ACTAGAATTAA AGGGATAAAA TAACAATGTG TGCATAATGA ACCCTATGAA ACMAACMMAA	360
GCTAGGTTTT TTTCATAGST CTTCTTCCAG ATTGAATGAA CGTCTGTTCT AAAATTAAAC	420
CCCCCAGGGAA AATATTCACT TAACTATGTT AAAAACCCAG ACTTGTGATT GAGTTTGCC	480
TGAAAATGCT TTCATAATTA TGTGTGAATG TGTGTC	516

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GTATAATGCA GGTGCTATAA GGTGAGCATG AGACACAGAT CTTTGCTTTC CACCCCTGTTC	60
TTCTTATGGT TGGGTATTCT TGTCACAGTA ACTTAACTGA TCTAGGAAAG AAAAAATGTT	120
T	121

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

TGGAGACTGG AACACAAC	18
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(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GTGTGGCCAG GGTAGAGAAC T	21
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(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ATCTCCGGCA GGCATATCT	19
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(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

TGAAATCACA GCCAAGATGA G

21

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CCATAGCCTG TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

CCATAGCCTA TTTCGTAGC

19

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2791 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

TGGGACAGGG AGCTCCGGGG TCCGCGGTTT CACATCGGAA ACAAAACAGC GGCTGGTCTG

60

GAAGGAAACCT GAGCTACGAG CCGCGGCGGC AGCGGGCGG CGGGGAAGCG TATACTAAT

120

CTGGGAGCCT GCAAGTGACA ACAGCCTTG CGGTCTTAG ACAGCTTGGC CTGGAGGAGA

180

ACACATGAAA GAAAGAACCT CAAGAGGCTT TGTTTCTGT GAAACAGTAT TTCTATACAG

240

TTGCTCCAAT GACAGAGTTA CCTGCACCGT TGTCTACTT CCAGAATGCA CAGATGTCTG

300

AGGACAACCA CCTGAGCAAT ACTGTACGTA GCCAGAATGA CAATAGAGAA CGGCAGGAGC	360
ACAACGACAG ACGGAGCCTT GGCCACCCCTG AGCCATTATC TAATGGACGA CCCCAGGGTA	420
ACTCCCAGCA GGTGGTGGAG CAAGATGAGG AAGAAGATGA GGAGCTGACA TTGAAATATG	480
GCGCCAAGCA TGTGATCATG CTCTTGTCC CTGTGACTCT CTGCATGGTG GTGGTCGTGG	540
CTACCATTA GTCAGTCAGC TTTTATACCC GGAAGGATGG GCAGCTAACATC TATAACCCAT	600
TCACAGAAGA TACCGAGACT GTGGGCCAGA GAGCCCTGCA CTCAATTCTG AATGCTGCCA	660
TCATGATCAG TGTCAATTGTT GTCATGACTA TCCTCCTGGT GGTTCTGTAT AAATACAGGT	720
GCTATAAGGT CATCCATGCC TGGCTTATTA TATCATCTCT ATTGTTGCTG TTCTTTTTT	780
CATTCAATTAA CTTGGGGAA GTGTTAAAAA CCTATAACGT TGCTGTGGAC TACATTACTG	840
TTGCACTCCT GATCTGGAAT TTTGGTGTGG TGGGAATGAT TTCCATTACAC TGGAAAGGTC	900
CACTTCGACT CCAGCAGGCA TATCTCATTA TGATTAGTGC CCTCATGGCC CTGGTGTAA	960
TCAAGTACCT CCCTGAATGG ACTGCGTGGC TCATCTTGGC TGTGATTCA GTATATGATT	1020
TAGTGGCTGT TTTGTGTCCG AAAGGTCCAC TTCGTATGCT GGTTGAAACA GCTCAGGAGA	1080
GAAATGAAAC GCTTTTCCA GCTCTCATTT ACTCCTCAAC AATGGTGTGG TTGGTGAATA	1140
TGGCAGAAGG AGACCCGGAA GCTCAAAGGA GAGTATCCAA AAATTCCAAG TATAATGCAG	1200
AAAGCACAGA AAGGGAGTCA CAAGACACTG TTGCAGAGAA TGATGATGGC GGGTCAGTG	1260
AGGAATGGGA AGCCCAGAGG GACAGTCATC TAGGGCCTCA TCGCTCTACA CCTGAGTCAC	1320
GAGCTGCTGT CCAGGAACCTT TCCAGCAGTA TCCTCGCTGG TGAAGACCCA GAGGAAAGGG	1380
GAGTAAAAC TGGATTGGGA GATTCATTT TCTACAGTGT TCTGGTTGGT AAAGCCTCAG	1440
CAACAGCCAG TGGAGACTGG AACACAACCA TAGCCTGTT CGTAGCCATA TTAATTGGTT	1500
TGTGCCTTAC ATTATTACTC CTTGCCATTT TCAAGAAAGC ATTGCCAGCT CTTCCAATCT	1560
CCATCACCTT TGGGCTTGTT TTCTACTTTG CCACAGATTA TCTTGTACAG CCTTTTATGG	1620
ACCAATTAGC ATTCCATCAA TTTTATATCT AGCATATTG CGGTTAGAAT CCCATGGATG	1680
TTTCTTCTTT GACTATAACC AAATCTGGGG AGGACAAAGG TGATTTCCCT GTGTCCACAT	1740
CTAACAAAGT CAAGATTCCC GGCTGGACTT TTGCAGCTTC CTTCCAAGTC TTCCGTACCA	1800
CCTTGCACCA TTGGACTTTG GAAGGAGGTG CCTATAGAAA ACGATTTGA ACATACTTCA	1860
TCGCAGTGGA CTGTGTCCCT CGGTGCAGAA ACTACCAGAT TTGAGGGACG AGGTCAAGGA	1920
GATATGATAG GCCCGGAAGT TGCTGTGCC CATCAGCAGC TTGACGCGTG GTCACAGGAC	1980
GATTTCACTG AACTGCGAA CTCTCAGGAC TACCGGTTAC CAAGAGGTTA GGTGAAGTGG	2040
TTTAAACCAA ACGGAACCTCT TCATCTTAAA CTACACGTTG AAAATCAACC CAATAATTCT	2100
GTATTAACG AATTCTGAAC TTTTCAGGAG GTACTGTGAG GAAGAGCAGG CACCAGCAGC	2160
AGAATGGGGAA ATGGAGAGGT GGGCAGGGGT TCCAGCTTCC CTTTGATTTT TTGCTGCAGA	2220

CTCATCCTTT TTAAATGAGA CTTGTTTCC CCTCTCTTG AGTCAAGTCA AATATGTAGA	2280
TTGCCTTGG CAATTCTCT TCTCAAGCAC TGACACTCAT TACCGTCTGT GATTGCCATT	2340
TCTTCCAAG GCCAGTCTGA ACCTGAGGTT GCTTTATCCT AAAAGTTTA ACCTCAGGTT	2400
CCAAATTCAAG TAAATTTGG AAACAGTACA GCTATTCTC ATCAATTCTC TATCATGTTG	2460
AAGTCAAATT TGGATTTCC ACCAAATTCT GAATTTGTAG ACATACTTGT ACGCTCACCT	2520
GCCCCCAGAT GCCTCCTCTG TCCTCATTCT TCTCTCCCAC ACAAGCAGTC TTTTCTACA	2580
GCCAGTAAGG CAGCTCTGTC TGGTAGCAGA TGGTCCCATT ATTCTAGGGT CTTACTCTT	2640
GTATGATGAA AAGAATGTGT TATGAATCGG TGCTGTCAGC CCTGCTGTCA GACCTTCTTC	2700
CACAGCAAAT GAGATGTATG CCCAAAGCGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG	2760
AAGCAAAAAA AAAAAAAA AAAAAAAA A	2791

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Thr Glu Leu Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
1 5 10 15

Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
20 25 30

Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
35 40 45

Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
50 55 60

Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
65 70 75 80

His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
85 90 95

Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
100 105 110

Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
115 120 125

Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Val Ile Val
130 135 140

Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
 145 150 155 160

Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
165 170 175

Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
 180 185 190
 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
 195 200 205
 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
 210 215 220
 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460
 Phe Tyr Ile
 465

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1964 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACCANACANC	GGCAGCTGAG	GCGGAAACCT	AGGCTGCGAG	CCGGCCGCC	GGGCAGCGGAG	60
AGAGAAGGAA	CCAACACAAG	ACAGCAGCCC	TTCGAGGTCT	TTAGGCAGCT	TGGAGGAGAA	120
CACATGAGAG	AAAGAATCCC	AAGAGGTTT	GTTTCTTG	AGAAGGTATT	TCTGTCCAGC	180
TGCTCCAATG	ACAGAGATAC	CTGCACCTT	GTCCTACTTC	CAGAATGCC	AGATGTCTGA	240
GGACAGCCAC	TCCAGCAGCG	CCATCCGGAG	CCAGAATGAC	AGCCAAGAAC	GGCAGCAGCA	300
GCATGACAGG	CAGAGACTTG	ACAACCCTGA	GCCAATATCT	AATGGGCGGC	CCCAGAGTAA	360
CTCAAGACAG	GTGGTGAAC	AAGATGAGGA	GGAAGACGAA	GAGCTGACAT	TGAAATATGG	420
AGCCAAGCAT	GTCATCATGC	TCTTGTC	CGTGACCTC	TGCATGGTC	TCGTCGTGGC	480
CACCATCAAA	TCAGTCAGCT	TCTATACCCG	GAAGGACGGT	CAGCTAATCT	ACACCCCATT	540
CACAGAAGAC	ACTGAGACTG	TAGGCCAAAG	AGCCCTGCAC	TCGATCCTGA	ATGCCGCCAT	600
CATGATCAGT	GTCATTGTCA	TTATGACCAT	CCTCCTGGTG	GTCCTGTATA	AATACAGGTG	660
CTACAAGGTC	ATCCACGCCT	GGCTTATTAT	TTCATCTCTG	TTGTTGCTGT	TCTTTTTTC	720
GTTCATTTAC	TTAGGGGAAG	TATTAAGAC	CTACAATGTC	GCCGTGGACT	ACGTTACAGT	780
AGCACTCCTA	ATCTGGAATT	TTGGTGTGGT	CGGGATGATT	GCCATCCACT	GGAAAGGCC	840
CCTTCGACTG	CAGCAGGCCT	ATCTCATTAT	GATCAGTGCC	CTCATGGCCC	TGGTATTTAT	900
CAAGTACCTC	CCCGAATGGA	CCGCATGGCT	CATCTGGCT	GTGATTTAG	TATATGATTT	960
GGTGGCTGTT	TTATGTC	AAGGCCACT	TCGTATGCTG	GTTGAAACAG	CTCAGGAAAG	1020
AAATGAGACT	CTCTTCCAG	CTCTTATCTA	TTCCCTAAC	ATGGTGTGGT	TGGTGAATAT	1080
GGCTGAAGGA	GACCCAGAAG	CCCAAAGGAG	GGTACCCAAG	AACCCCAAGT	ATAACACACA	1140
AAGAGCGGAG	AGAGAGACAC	AGGACAGTGG	TTCTGGAAC	GATGATGGTG	GCTCAGTGA	1200
GGAGTGGAG	GCCCAAAGAG	ACAGTCACCT	GGGGCCTCAT	CGCTCCACTC	CCGAGTCAAG	1260
AGCTGCTGTC	CAGGAAC	CTGGGAGCAT	TCTAACGAGT	GAAGACCCGG	AGGAAAGAGG	1320
AGTAAAACCTT	GGACTGGAG	ATTTCA	CTACAGTGT	CTGGTTGGTA	AGGCCTCAGC	1380
AACCGCCAGT	GGAGACTGGA	ACACAACC	AGCCTGCTT	GTAGCCATAC	TGATCGGCCT	1440
GTGCCTTACA	TTACTCCTGC	TCGCCATT	CAAGAAAGCG	TTGCCAGCCC	TCCCCATCTC	1500
CATCACCTTC	GGGCTCGTGT	TCTACTTCGC	CACGGATTAC	CTTGTGCAGC	CCTTCATGGA	1560
CCAACCTGCA	TTCCATCAGT	TTTATATCTA	GCCTTCTGC	AGTTAGAAC	TGGATGTTTC	1620
TTCTTGATT	ATCAAAAACA	CAAAACAGA	GAGCAAGCCC	GAGGAGGAGA	CTGGTGACTT	1680
TCCTGTC	TCAGCTAAC	AAGGCAGGAC	TCCAGCTGGA	CTTCTGCAGC	TTCCCTCCGA	1740
GTCTCCCTAG	CCACCCGCAC	TACTGGACTG	TGGAAGGAAG	CGTCTACAGA	GGAACGGTTT	1800

CCAACATCCA TCGCTGCAGC AGACGGTGTC CCTCAGTGAC TTGAGAGACA AGGACAAGGA	1860
AATGTGCTGG GCCAAGGAGC TGCCGTGCTC TGCTAGCTTT GACCGTGGGC ATGGAGATTT	1920
ACCCGCACTG TGAACCTCTCT AAGGTAAACA AAGTGAGGTG AACC	1964

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 467 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met			
1	5	10	15
Ser Glu Asp Ser His Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser			
20	25	30	
Gln Glu Arg Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu			
35	40	45	
Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu			
50	55	60	
Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys			
65	70	75	80
His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val			
85	90	95	
Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln			
100	105	110	
Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg			
115	120	125	
Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val			
130	135	140	
Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys			
145	150	155	160
Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe			
165	170	175	
Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala			
180	185	190	
Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val			
195	200	205	
Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala			
210	215	220	

Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
 225 230 235 240
 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
 245 250 255
 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
 305 310 315 320
 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
 355 360 365
 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460
 Phe Tyr Ile
 465

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCA CGAGGGCATT TCCAGCAGTG AGGAGACAGC CAGAAGCAAG CTTTTGGAGC 60

TGAAGGAACC	TGAGACAGAA	GCTAGTCCCC	CCTCTGAATT	TTACTGATGA	AGAAACTGAG	120
GCCACAGAGC	TAAAGTACT	TTTCCCAAGG	TCGCCAGCG	AGGACGTGGG	ACTTCTCAGA	180
CGTCAGGAGA	GTGATGTGAG	GGAGCTGTGT	GACCATAGAA	AGTACGTGT	AAAAAACAG	240
CGCTGCCCTC	TTTGAAAGCC	AGGGAGCAGC	ATTCAATTAG	CCTGCTGAGA	AGAAGAAACC	300
AAGTGTCCGG	GATTCAAGAC	CTCTCTGCCG	CCCCAAGTGT	TCGTGGTGCT	TCCAGAGGCA	360
GGGCTATGCT	CACATTCACTG	GCCTCTGACA	GCGAGGAAGA	AGTGTGTGAT	GAGCGGACGT	420
CCCTAATGTC	GGCCGAGAGC	CCCACGCCGC	GCTCCTGCCA	GGAGGGCAGG	CAGGGCCAG	480
AGGATGGAGA	GAATACTGCC	CAGTGGAGAA	GCCAGGAGAA	CGAGGAGGAC	GGTGAGGAGG	540
ACCCCTGACCG	CTATGTCTGT	AGTGGGGTTC	CCGGGCGGCC	GCCAGGCCTG	GAGGAAGAGC	600
TGACCCCTCAA	ATACGGAGCG	AAGCATGTGA	TCATGCTGTT	TGTGCCTGTC	ACTCTGTGCA	660
TGATCGTGGT	GGTAGGCCACC	ATCAAGTCTG	TGCGCTTCTA	CACAGAGAAG	AATGGACAGC	720
TCATCTACAC	GCCATTCACT	GAGGACACAC	CCTCCGTGGG	CCAGGCCCTC	CTCAACTCCG	780
TGCTGAACAC	CCTCATCATG	ATCAGCGTCA	TCGTGGTTAT	GACCATCTTC	TTGGTGGTGC	840
TCTACAAGTA	CCGCTGCTAC	AAGTTCATCC	ATGGCTGGTT	GATCATGTCT	TCACTGATGC	900
TGCTGTTCCCT	CTTCACCTAT	ATCTACCTTG	GGGAAGTGCT	CAAGACCTAC	AATGTGGCCA	960
TGGACTACCC	CACCCCTTTG	CTGACTGTCT	GGAACTTCGG	GGCAGTGGGC	ATGGTGTGCA	1020
TCCACTGGAA	GGGCCCTCTG	GTGCTGCAGC	AGGCCTACCT	CATCATGATC	AGTGCCTCA	1080
TGGCCCTAGT	GTTCATCAAG	TACCTCCCAG	AGTGGTCCGC	GTGGGTCATC	CTGGGCGCCA	1140
TCTCTGTGTA	TGATCTCGTG	GCTGTGCTGT	GTCCCAAAGG	GCCTCTGAGA	ATGCTGGTAG	1200
AAACTGCCCA	GGAGAGAAAT	GAGCCCATAT	TCCCTGCCCT	GATATACTCA	TCTGCCATGG	1260
TGTGGACGGT	TGGCATGGCG	AAGCTGGACC	CCTCCTCTCA	GGGTGCCCTC	CAGCTCCCT	1320
ACGACCCGGA	GATGGAAGAA	GACTCCTATG	ACAGTTTGG	GGAGCCTTCA	TACCCCGAAG	1380
TCTTGAGCC	TCCCTTGACT	GGCTACCCAG	GGGAGGAGCT	GGAGGAAGAG	GAGGAAAGGG	1440
GCGTGAAGCT	TGGCCTCGGG	GACTTCATCT	TCTACAGTGT	GCTGGTGGGC	AAGGCGGCTG	1500
CCACGGGCAG	CGGGGACTGG	AATACCACGC	TGGCCTGCTT	CGTGGCCATC	CTCATTGGCT	1560
TGTGTCTGAC	CCTCCTGCTG	CTTGCTGTGT	TCAAGAAGGC	GCTGCCGCC	CTCCCCATCT	1620
CCATCACGTT	CGGGCTCATC	TTTACTTCT	CCACGGACAA	CCTGGTGCAG	CCGTTCATGG	1680
ACACCCTGGC	CTCCCATCAG	CTCTACATCT	GAGGGACATG	GTGTGCCACA	GGCTGCAAGC	1740
TGCAGGGAAT	TTTCATTGGA	TGCAGTTGTA	TAGTTTACA	CTCTAGTGCC	ATATATTTTT	1800
AAGACTTTTC	TTTCCTTAAA	AAATAAAGTA	CGTGTAACT	TGGTGAGGAG	GAGGCAGAAC	1860
CAGCTTTTG	GTGCCAGCTG	TTTCATCACC	AGACTTTGGC	TCCCGCTTTG	GGGAGCGCCT	1920
CGCTTCACGG	ACAGGAAGCA	CAGCAGGTTT	ATCCAGATGA	ACTGAGAAGG	TCAGATTAGG	1980

GTGGGGAGAA GAGCATCCGG CATGAGGGCT GAGATGCCA AAGAGTGTGC TCGGGAGTGG	2040
CCCCTGGCAC CTGGGTGCTC TGGCTGGAGA GGAAAAGCCA GTTCCCTACG AGGAGTGTTC	2100
CCAATGCTTT GTCCATGATG TCCTTGTAT TTTATTNCCY TTANAAACTG ANTCCNTTN	2160
TTNTTDCGGC AGTCACMCTN CTGGGRAGTG GCTTAATAGT AANATCAATA AANAGNTGAG	2220
TCCTNTTAGA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	2280
AAAAA	2285

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu	
1 5 10 15	
Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln	
20 25 30	
Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg	
35 40 45	
Ser Gln Glu Asn Glu Glu Asp Gly Glu Asp Pro Asp Arg Tyr Val	
50 55 60	
Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr	
65 70 75 80	
Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr	
85 90 95	
Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr	
100 105 110	
Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr	
115 120 125	
Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile	
130 135 140	
Met Ile Ser Val Ile Val Val Met Thr Ile Phe Leu Val Val Leu Tyr	
145 150 155 160	
Lys Tyr Arg Cys Tyr Lys Phe Ile His Gly Trp Leu Ile Met Ser Ser	
165 170 175	
Leu Met Leu Leu Phe Leu Phe Thr Tyr Ile Tyr Leu Gly Glu Val Leu	
180 185 190	

Lys Thr Tyr Asn Val Ala Met Asp Tyr Pro Thr Leu Leu Leu Thr Val
 195 200 205
 Trp Asn Phe Gly Ala Val Gly Met Val Cys Ile His Trp Lys Gly Pro
 210 215 220
 Leu Val Leu Gln Gln Ala Tyr Leu Ile Met Ile Ser Ala Leu Met Ala
 225 230 235 240
 Leu Val Phe Ile Lys Tyr Leu Pro Glu Trp Ser Ala Trp Val Ile Leu
 245 250 255
 Gly Ala Ile Ser Val Tyr Asp Leu Val Ala Val Leu Cys Pro Lys Gly
 260 265 270
 Pro Leu Arg Met Leu Val Glu Thr Ala Gln Glu Arg Asn Glu Pro Ile
 275 280 285
 Phe Pro Ala Leu Ile Tyr Ser Ser Ala Met Val Trp Thr Val Gly Met
 290 295 300
 Ala Lys Leu Asp Pro Ser Ser Gln Gly Ala Leu Gln Leu Pro Tyr Asp
 305 310 315 320
 Pro Glu Met Glu Glu Asp Ser Tyr Asp Ser Phe Gly Glu Pro Ser Tyr
 325 330 335
 Pro Glu Val Phe Glu Pro Pro Leu Thr Gly Tyr Pro Gly Glu Glu Leu
 340 345 350
 Glu Glu Glu Glu Glu Arg Gly Val Lys Leu Gly Leu Gly Asp Phe Ile
 355 360 365
 Phe Tyr Ser Val Leu Val Gly Lys Ala Ala Ala Thr Gly Ser Gly Asp
 370 375 380
 Trp Asn Thr Thr Leu Ala Cys Phe Val Ala Ile Leu Ile Gly Leu Cys
 385 390 395 400
 Leu Thr Leu Leu Leu Ala Val Phe Lys Lys Ala Leu Pro Ala Leu
 405 410 415
 Pro Ile Ser Ile Thr Phe Gly Leu Ile Phe Tyr Phe Ser Thr Asp Asn
 420 425 430
 Leu Val Arg Pro Phe Met Asp Thr Leu Ala Ser His Gln Leu Tyr Ile
 435 440 445

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGTACCGCCA CCATGACAGA GGTACCTGCA C

31

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCACTG GCTGTAGAAA AAGAC

25

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GGATCCGGTC CACTTCGTAT GCTG

24

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTTTTGAAAT TCTTAGGCTA TGGTTGTGTT CCA

33

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GATTAGTGGT TGTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GATTAGTGGC TGTTTGTG

19

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

TTTTTCCAGC TCTCATTAA

19

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

TTTTTCCAGT TCTCATTAA

19

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TACAGTGTTC TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

TACAGTGTTC TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

TACAGTGTG TGGTTGGTA

19

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GTCTAGATAA GNCAACATTC AGGGGTAGAA GGGGACTGTT TATTTTTTCC TTTAGTCTCT

60

CTTAAAGAGT GAGAAAAATT TTCCCAGGAA TCCCGGTGGA CTTTGCTTCA CCACTCATAG

120

GTTCATACCA AGTTACAACC CCACAACCTT AGAGCTTTG TTAGGAAGAG GCTTGGTGGG

180

ATTACCGTGC TTGGCTTGGC TTGGTCAGGA TTCACCCACCA GAGTCATGTG GGAGGGGGTG

240

GGAACCCAAA CAATTCAAGGA TTCTGCCCTC AGGAAATAAA GGAGAAAATAA GCTGTTGGAT

300

AAACTACCAG CAGGCAC TGC TACAGCCC AT GCTTTGTGGT TTAAGGGCCA GCTAGTTACA	360
ATGACAGCTA GTTACTGTTT CCATGTAATT TTCTTAAAGG TATTAAATTT TTCTAAATAT	420
TAGAGCTGTA ACTTCCACTT TCTCTTGAAG GCACAGWAAG GGAGTCACAA GACACTGTTG	480
CAGAGAATGA TGATGGCGGG TTCAGTGAGG AATGGGAASC CCAGRGGGAC ANTCACTAG	540
GGCCTCATCG CTCTACACCT GAGTCACGAG CTKCTNTCCA GGRAC TTTCC ANCAGTATCC	600
TCGCTGGTGA AGACCCAGAG GAAAGNATGT TCANTTCTCC ATNTTTCAAA GTCATGGATT	660
CCTTTAGGTA GCTACATTAT CAACCTTTT GAGAATAAAA TGAATTGAGA GTGTTACAGT	720
CTAATTCTAT ATCACATGTA ACTTTTATTG GGATATATCA GTAATAGTGC TTTTYNTTT	780
TTTTTTTTT TTTTTTTTT TTTTNGGNGA NAGAGTCTCG CTCTGTCGCC AGGTTGGAGT	840
GCAATGGTGC GATCTGGCT CACTGAAAGC TCCACCNC C GGGTTCAAGT GATTCTCCTG	900
CCTCAGCCNC CCAAGTAGNT GGGACTACAG GGGTGCGCCA CCACGCCTGG GATAATTTG	960
GGNTTTTTAG TAGAGATGGC GTTTCACCAN CTTGGNGCAG GCTGGTCTTG GAACTCCTGA	1020
NATCATGATC TGCCTGCCTT AGCCTCCCCA AAGTGCTGGG ATTNCAGGGG TGAGCCACTG	1080
TTCTGGGCC TC	1092

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1003 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CTGCAGTGAG CCGAGATCAT GCTGCTGTAC TCCAGCCTGG GCCACAGAGC CAAACTCCAT	60
CTCCCCAAAAA AAAAAAATAT TAATTAATAT GATNAAATGA TGCCTATCTC AGAATTCTTG	120
TAAGGATTTC TTGKACAAG TGCTGGGTAT AACTATANA TTCACTAGAT GNCGATTATT	180
ACTTAYTATT GTTATTGATA AATAACAGCA GCATCTACAG TTAAGACTCC AGAGTCAGTC	240
ACATAGAAC TGGNACTCCT ATTGTAGNAA ACCCNMMAG AAAGAAAACA CAGCTGAAGC	300
CTAATTTGT ATATCATTAA CTGACTTCTC TCATTCATTG TGGGGTTGAG TAGGGCAGTG	360
ATATTTTGAA ATTGTGAAAT CATANCAAAG AGTGACCAAC TTTTTAATAT TTGTAACCTT	420
TCCTTTTTAG GGGGAGTAAA ACTTGGATTG GGAGATTCA TTTTCTACAG TGTCTGGTT	480
GGTAAAGCCT CAGCAACAGC CAGTGGAGAC TGGAACACAA CCATAGCCTG TTTCGTAGCC	540
ATATTAATTG TMMSTATAACA CTAATAAGAA TGTGTCAGAG CTCTTAATGT CMAAACTTG	600
ATTACACAGT CCCTTTAAGG CAGTTCTGTT TTAACCCAG GTGGGTTAAA TATTCCAGCT	660
ATCTGAGGAG CTTTNGATA ATTGGACCTC ACCTTAGTAG TTCTCTACCC TGGCCACACA	720

TTAGAACATCAC TTGGGAGCTT TTAAAAGCTGT AAGCTCTGCC CTGAGATATT CTTACTCAAT	780
TTAATTGTGT AGTTTTAAA ATTCCCCAGG AAATTCTGGT ATTTCTGTTT AGGAACCGCT	840
GCCTCAAGCC TAGCAGCACA GATATGTAGG AAATTAGCTC TGTAAGGTTG GTCTTACAGG	900
GATAAACAGA TCCTTCCTTA GTCCCTGGAC TTAATCACTG AGAGTTGGG TGGTGGTTT	960
GGATTTAATG ACACAAACCTG TAGCATGCAG TGTTACTTAA GAC	1003

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1726 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGATCCCTCC CCTTTTAAAGA CCATACAAGG TAACCTCCGG ACGTTGCCAT GGCATCTGTA	60
AACTGTCATG GTGTTGGCGG GGAGTGTCTT TTAGCATGCT AATGTATTAT AATTAGCGTA	120
TAGTGACCGAG TGAGGATAAAC CAGAGGTAC TCTCCTCACC ATCTGGTTT TGGTGGGTTT	180
TGGCCAGCTT CTTTATTGCA ACCAGTTTA TCAGCAAGAT CTTTATGAGC TGTATCTTGT	240
GCTGACTTCC TATCTCATCC CGNAACTAAC AGTACCTAAC CTCCTGAAA TTGMAGNCCA	300
GNAGGTCTTG GNCTTATTTN ACCCAGCCCC TATTCAARAT AGAGTNGYTC TTGGNCCAAA	360
CGCCYCTGAC ACAAGGATTT TAAAGTCTTA TTAATTAAGG TAAGATAGKT CCTTGSATAT	420
GTGGTCTGAA ATCACAGAAA GCTGAATTG GAAAAAGGTG CTTGGASCTG CAGCCAGTAA	480
ACAAGTTTC ATGCAGGTGT CAGTATTTAA GGTACATCTC AAAGGATAAG TACAATTGTG	540
TATGTTGGGA TGAACAGAGA GAATGGAGCA ANCCAAGACC CAGGTAAAAG AGAGGACCTG	600
AATGCCTTCA GTGAACAATG ATAGATAATC TAGACTTTA AACTGCATAC TTCCTGTACA	660
TTGTTTTTC TTGCTTCAGG TTTTTAGAAC TCATAGTGAC GGGTCTGTTG TTAATCCCAG	720
GTCTAACCGT TACCTTGATT CTGCTGAGAA TCTGATTTAC TGAAAATGTT TTTCTTGTGC	780
TTATAGAATG ACAATAGAGA ACGGCAGGAG CACAACGACA GACGGAGCCT TGGCCACCC	840
GANCCATTAT CTAATGGACG ACCCAGGGTA ACTCCCGGCA GGTGGTGGAN CAAGATGAGG	900
AAGAAGATGA GGANCTGACA TTGAAATATG NCGSCAAGCA TGTGATCATG CTCTTGKCC	960
CTGTGACTCT CTGCATGGTG GTGGTCGTGG NTACCATTAA GTCAGTCAGC TTTTATACCC	1020
GGAAGGATGG GCAGCTGTAC GTATGAGTTT KGTTTTATTA TTCTCAAASC CAGTGTGGCT	1080
TTCTTTACA GCATGTCATC ATCACCTTGA AGGCCTCTNC ATTGAAGGGG CATGACTTAG	1140
CTGGAGAGGCC CATCCTCTGT GATGGTCAGG AGCAGTTGAG AGANCGAGGG GTTATTACTT	1200
CATGTTTAA GTGGAGAAAA GGAACACTGC AGAAGTATGT TTCCTGTATG GTATTACTGG	1260

ATAGGGCTGA AGTTATGCTG AATTGAACAC ATAAATTCTT TTCCACCTCA GGGNCATTGG	1320
GCGCCCATTG NTCTTCTGCC TAGAATATTTC TTTCCCTTNC TNACTTKGGN GGATTAATT	1380
CCTGTCATCC CCCTCCTCTT GGTGTTATAT ATAAAGTNTT GGTGCCGCAA AAGAAGTAGC	1440
ACTCGAATAT AAAATTTC TTTAATTCT CAGCAAGGNA AGTTACTTCT ATATAGAAGG	1500
GTGCACCCNT ACAGATGGAA CAATGGCAAG CGCACATTG GGACAAGGGA GGGGAAAGGG	1560
TTCTTATCCC TGACACACGT GGTCCNGCT GNTGTGTNCT NCCCCACTG ANTAGGGTTA	1620
GAUTGGACAG GCTTAAACTA ATTCCAATTG GNTAATTAA AGAGAATNAT GGGGTGAATG	1680
CTTTGGGAGG AGTCAAGGAA GAGNAGGTAG NAGGTAACCTT GAATGA	1726

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CNCGTATAAA AGACCAACAT TGCCANCNAC AACCACAGGC AAGATCTTCT CCTACCTTCC	60
CCCNNGGTGT AATACCAAGT ATTNCNAAT TTGTGATAAA CTTTCATTGG AAAGTGACCA	120
CCCTCCTTGG TTAATACATT GTCTGTGCCT GCTTCACAC TACAGTAGCA CAGTTGAGTG	180
TTTGCCTGG AGACCATATG ACCCATAGAG CTTAAAATAT TCAGTCTGGC TTTTACAGA	240
GATGTTTCTG ACTTTGTTAA TAGAAAATCA ACCCAACTGG TTTAAATAAT GCACATACTT	300
TCTCTCTCAT AGAGTAGTGC AGAGGTAGNC AGTCCAGATT AGTASGGTGG CTTCACGTT	360
ATCCAAGGAC TCAATCTCCT TCTTTCTTCT TTAGCTTCTA ACCTCTAGCT TACTTCAGGG	420
TCCAGGCTGG AGCCCTASCC TTCATTTCTG ACAGTAGGAA GGAGTAGGGG AGAAAAGAAC	480
ATAGGACATG TCAGCAGAAT TCTCTCCTTA GAAGTTCCAT ACACAACACA TCTCCCTAGA	540
AGTCATTGCC CTTACTTGTGTT CTCATAGCCA TCCTAAATAT AAGGGAGTCA GAAGTAAAGT	600
CTKKNTGGCT GGGAAATATTG GCACCTGGAA TAAAAATGTT TTTCTGTGAA TGAGAAACAA	660
GGGGAAGATG GATATGTGAC ATTATCTTAA GACAACCTCA GTTGCAATTA CTCTGCAGAT	720
GAGAGGCACT AATTATAAGC CATATTACCT TTCTCTGAC AACCACTGT CAGCCNCGT	780
GGTTTCTGTG GCAGAATCTG GTTCYATAMC AAGTCCTAA TAANCTGTAS CCNAAAAAAT	840
TTGATGAGGT ATTATAATTA TTTCAATATA AAGCACCCAC TAGATGGAGC CAGTGTCTGC	900
TTCACATGTT AAGTCCTTCT TTCCATATGT TAGACATTG CTTTGAAGCA ATTTAGAGT	960
GTAGCTGTTT TTCTCAGGTT AAAAATTCTT AGCTAGGATT GGTGAGTTGG GGAAAAGTGA	1020
CTTATAAGAT NCGAATTGAA TTAAGAAAAA GAAAATTCTG TGTTGGAGGT GGTAATGTGG	1080

KTGGTGATCT YCATTAACAC TGANCTAGGG CTTKGKGTT TGKTTTATTG TAGAATCTAT	1140
ACCCCATTCA NAGAAGATAC CGAGACTGTG GGCCAGAGAG CCCTGCACTC AATTCTGAAT	1200
GCTGCCATCA TGATCAGNGT CATTGTWGTC ATGACTANN C TCCTGGTGGT TCWGTATAAA	1260
TACAGGTGCT ATAAGGTGAG CATGAGACAC AGATCTTGN TTTCCACCC GTTCTTCTTA	1320
TGGTTGGGTA TTCTTGTAC AGTAACCTAA CTGATCTAGG AAAGAAAAAA TGTTTGTCT	1380
TCTAGAGATA AGTTAATT TT TAGTTTCTT CCTCCTCACT GTGGAACATT CAAAAAAATAC	1440
AAAAAGGAAG CCAGGTGCAT GTGTAATGCC AGGCTCAGAG GCTGAGGCAG GAGGATCGCT	1500
TGGGCCAGG AGTCACAAG CAGCTTGGC AACGTAGCAA GACCCTGCCT CTATTAAGA	1560
AAACAAAAAA CAAATATTGG AAGTATTAA TATGCATGGA ATCTATATGT CATGAAAAAA	1620
TTAGTGTAAA ATATATATAT TATGATTAGN TATCAAGATT TAGTGATAAT TTATGTTATT	1680
TTGGGATTTC AATGCCTTT TAGGCCATTG TCTCAAMAAA TAAAAGCAGA AAACAAAAAA	1740
AGTTGTAAC GAAAAATAAA CATTCCATA TAATAGCACA ATCTAAGTGG GTTTTGNTT	1800
GTTTGTGTTG TTGTTGAAGC AGGGCCTTGC CCTNYCACCC AGGNTGGAGT GAAGTGCAGT	1860
GGCACGATTT TGGCTCACTG CAG	1883

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGTTTGACA ATTTCTCCGT TCCACCCCTTG ATTAATAAG GTAGTATTCA TTTTTTAAGT	60
TTTAGCTTTT GGATATATGT GTAAGTGTGG TATGCTGTCT AATGAATTAA GACAATTGGT	120
NCTKTCTTTA CCCMACANCT GGACMAAGAG CAGGCAAGAT NCAANAATCA AGTGACCCAG	180
NCAAACCAGA CACATTTCT GCTCTCAGCT AGCTTGCCAC CTAGAAAGAC TGGTTGTCNA	240
AGTTGGAGTC CAAGAATCGC GGAGGATGTT TAAAATGCAG TTTCTCAGGT TCTCNCCACC	300
CACCAGAAGT TTTGATTCA TGAGTGGTGG GAGAGGGCAG AGATATTGC GATTTAACAA	360
GCATTCTCTT GATTGTGATG CAGCTGGTTC SCAAATAGGT ACCCTAAAGA AATGACAGGT	420
GTAAATTTA GGATGCCAT CGCTTGTATG CCGGGAGAAG CACACGCTGG GCCCAATTAA	480
TATAGGGGCT TTCGTCCTCA GCTCGAGCAR CCTCAGAACCC CGACAAACCCY ACGCCAGCKC	540
TCTGGGCGGA TTCCRTCAAGK TGGGGAGSC CAGGTGGAGC TCTGGKTTCT CCCCGCAATC	600
GTTTCTCCAG GCCGGAGGCC CCGCCCCCTT CCTCCTGGCT CCTCCCCCTCC TCCGTGGGCC	660

GNCCGCCAAC GACGCCAGAG CCGGAAATGA CGACAACGGT GAGGGTTCTC GGGCGGGGCC	720
TGGGACAGGC AGCTCCGGGG TCCNCNNWT NACATCGAA ACAAAACAGC GGCTGGTCTG	780
GAAGGAACCT GAKCTACGAC CCGCGCGGC AGCGGGCGG CGGGGAAGCG TATGTGCGTG	840
ATGGGGAGTC CGGGCAAGCC AGGAAGGCAC CGCGGACATG GGCGGCCGCG GGCAGGGNCC	900
GGNCCTTGT GGCGCCCGG GCCGCGAAGC CGGTGTCCTA AAAGATGAGG GGCGGGCGC	960
GGCCGGTGG GGCTGGGAA CCCCGTGTGG GAAACCAGGA GGGCGGCCG TTTCCTCGGG	1020
CTTCGGGCGC GGCGGGTGG AGAGAGATTG CGGGGAGCCT TGGTCCGGAA ATGCTGTTG	1080
CTCGAAGACG TCTCAGGGCG CAGGTGCCTT GGGCCGGAT TAGTAGCCGT CTGAACCTGGA	1140
GTGGAGTAGG AGAAAGAGGA AGCGTCTTGG GCTGGGTCTG CTTGAGCAAC TGGTGAAACT	1200
CCGCGCCTCA CGCCCCGGGT GTGTCCTTGT CCAGGGCGA CGAGCATTCT GGGCGAAGTC	1260
CGCACGCCTC TTGTCGAGG CGGAAGACGG GGTCTTGATG CTTTCTCCTT GGTGGGACT	1320
GTCTCGAGGC ATGCATGTCC AGTGACTION GTGTTGCTG CTGCTTCCCT CTCAGATTCT	1380
TCTCACCGTT GTGGTCAGCT CTGCTTCTAGG CATATTAATC CATACTGGAG GCTGGGATGG	1440
GTGAGAGAAT TGAGGTGACT TTTCCATAAT TCAGGTGAGA TGTGATTAGA GTYCGGATCC	1500
TNCGGTGGTG GCAGAGGCTT ACCAAGAAC ACTAACGGGA CATGGGAACC AATTGAGGAT	1560
CCAGGGAAATA AAGTGTGAAG TTGACTAGGA GGTTTCAGT TTAAGAACAT GGCAGAGACA	1620
TTCTCAGAAA TAAGGAAGTT AGGAAGAAAG ACCTGGTTA GAGAGGAGGG CGAGGAAGTG	1680
GTGGAAAGT GTCACCTTGG AAGTGCCAGC AGGTGAAAT GCCCTGTGAA CAGGACTGG	1740
GCTGAAAACA GGAATCAATT CCATAGATT CCAGTTGATG TTGGAGCAGT GGAGAAGTCT	1800
AANCTAAGGA AGGGGAAGAG GAGGCCAAGC CAAACACTTA GGAACACTTN CNACGAGGG	1860
GTGGAAGAAG AGCAAGGAGC CAGCTGAGGA GAATGAGTGT GGTTGGAGAA CCACCAACAGC	1920
NCAGGGTCGC CAGANCTGAG GAAGGGAGG GAAGCTTATC GAGKAMSGWC RACMKCGAGT	1980
TGGCAGGGAT	1990

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 736 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTCTTCCAC AGAGTTGTG CCTTACATTA TTACTCCTG CCATTTCAA	60
GAAAGCATTG TCAGCTCTTC CAATCTCCAT CACCTTGAGG CTTGTTTCT ACTTGCCAC	120
AGATTATCTT GTACAGCCTT TTATGGACCA ATTAGCATTC CATCAATTAT ATATCTAGCA	180

TATTTGCGGT TAGAACCCCA TGGATGTTTC TTCTTGACT ATAACAAAAT CTGGGGAGGA	240
CAAAGGTGAT TTCCTGTGTC CACATCTAAC AAATCAAGAT CCCCCGGCTGG ACTTTGGAG	300
GTTCCCTCCA AGTCTTCCTG ACCACCTTGC ACTATTGGAC TTTGGAAGGA GGTGCCCTATA	360
GAAAACGATT TTGAACATAC TTCATCGCAG TGGACTGTGT CCTCGGTGCA GAAACTACCA	420
GATTTGAGGG ACGAGGTCAA GGAGATATGA TAGGCCCGGA AGTTGCTGTG CCCCATCAGC	480
AGCTTGACGC GTGGTCACAG GACGATTTTC ACTGACACTG CGAACTCTCA GGACTACCGT	540
TACCAAGAGG TTAGGTGAAG TGGTTAAAC CAAACGGAAC TCTTCATCTT AAACTACACG	600
TTGAAAATCA ACCCAATAAT TCTGTATTAA CTGAATTCTG AACTTTCAAG GAGGTACTGT	660
GAGGAAGAGC AGGCACCACC AGCAGAATGG GGAATGGAGA GGTGGGCAGG GGTTCCAGCT	720
TCCCTTTGAT TTTTG	736

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGATCCGCC GCCTTGGCCT CCCAAAGTGC TGGGATTACA GGCATGAGCC ACCGCTCCTG	60
GCTGAGTCTG CGATTTCTTG CCAGCTCTAC CCAGTTGTGT CATCTTAAGC AAGTCACTGA	120
ACTTCTCTGG ATTCCCTTCT CCTNNWGTAA AATAAGNATG TTATCTGNCC NNCCTGCCTT	180
GGGCATTGTG ATAAGGATAA GATGACATTA TAGAATNTNG CAAAATTAAA AGCGCTAGAC	240
AAATGATTTT ATGAAAATAT AAAGATTAGN TTGAGTTGG GCCAGCATAG AAAAAAGGAAT	300
GTTGAGAACCA TTCCNTTAAG GATTACTCAA GCYCCCCTT TGSTGKNWAA TCAGANNGTC	360
ATNNAMNTAT CNTNTGTGGG YTGAAAATGT TTGGTTGTCT CAGGCGGTTC CTACTTATTG	420
CTAAAGAGTC CTACCTTGAG CTTATAGTAA ATTTGTCAGT TAGTTGAAAG TCGTGACAAA	480
TTAATACATT CCTGGTTTAC AAATTGGTCT TATAAGTATT TGATTGGTNT AAATGNATTT	540
ACTAGGATTT AACTAACAAAT GGATGACCTG GTGAAATCCT ATTTCAGACC TAATCTGGGA	600
GCCTGCAAGT GACAACAGCC TTTGCGGTCC TTAGACAGCT TGGCCTGGAG GAGAACACAT	660
GAAAGAMMGG TTTGWNTCTG NTTAWTGTAA TCTATGRAAG TGTTTTWAT MACAGTATAA	720
TTGTMTGMAC AAAGTTCTGT TTTTCTTTCC CTTTNCAGAA CCTCAAGAGG CTTTGTTTTC	780
TGTGAAACAG TATTCTATA CAGNTGCTCC AATGACAGAG TNACCTGCAC CGTTGTCTA	840
CTTCCAGAAT GCACAGATGT CTGAGGACAA CCACCTGAGC AATACTGTAC GTAGCCAGGT	900
ACAGCGTCAG TYTCTNAAAC TGCCTYYGNC AGACTGGATT CACTTATCAT CTCCCCTCAC	960

CTCTGAGAAA TGCTGAGGGG GSTAGGNAGG GCTTTCTCTA CTTNACCACA TTTNATAATT	1020
ATTTTGCGGT GACCTTCAGC TGATCGCTGG GAGGGACACA GGGCTTNTTT AACACATAGG	1080
GTGTTGGATA CAGNCCCTCC CTAATTACACA TTTCANC	1117

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CTGCAGCTTT CCTTTAAACT AGGAAGACTT GTTCCTATAC CCCAGTAACG ATACACTGTA	60
CACTAAGCAA ATAGCAGTCA AACCCAAATG AAATTTNTAC AGATGTTCTG TGTCATTTA	120
TNTTGTTTAT GTTGTCTCCC CCACCCCCAC CAGTCACCT GCCATTTATT TCATATTCAT	180
TCAACGTCTN NNTGTGTAAA AAGAGACAAA AAACATTAAA CTTTTTCCT TCGTTAATTC	240
CTCCCTACCA CCCATTACA AGTTTAGCCC ATACATTTA TTAGATGTCT TTTATGTTTT	300
TCTTTTNCTA GATTTAGTGG CTGTTNGTG TCCGAAAGGT CCACCTCGTA TGCTGGTTGA	360
AACAGCTCAG GAGAGAAATG AAACGCTTT TCCAGCTCTC ATTTACTCCT GTAAGTATTT	420
GGAGAATGAT ATTGAATTAG TAATCAGNGT AGAATTATC GGGAACTTGA AGANATGTNA	480
CTATGGCAAT TTCANGGNAC TTGTCTCATC TTAAATGANA GNATCCCTGG ACTCCTGNAG	540

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCCCGTCNAT GCATACTTG TGTGTCCAGT GCTTACCTGG AATCCNGTCT TTCCCAACAG	60
CAACAATGGT GTGGTTGGTG AATATGGCAG AAGGAGACCC GGAAGCTCAA AGGAGAGTAT	120
CCAAAAATTC CAAGTATAAT GCAGAAAGTA GGTAACYYYY NTTAGATAMN ATCTTGATTT	180
TNCAGGGTCA CTGTTATAAG CTAACAGTAT AGNAATGTTT TTATCGTCTT TCTNKGGNCA	240
TAGACTCCTN KGAGAATCTC TTGAGAACTA TGATAATGCC CAGTAAATAC NCAGATAAGT	300
ATTTAAGGAG TNCAGATACT CAAANCCAA CAATACNGTC AAAGCATCCT AGGTTAAGAC	360

AMCNCCCATT AAATACAGAA TACCAGCATG GAAAGGTTCA GGCTGAGGTT ATGATTGGGT	420
TTGGGTTTTG GGNNGNTTT TTATAAGTCA TGATTTAAA AAGAAAAAAAT AAACCTCTCTC	480
CAAACATGTA AAAGTAAGAA TCTCCTAAA	509

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CAGGAGTGGAA CTAGGTAAAT GNAAGNTGTT TTAAAGAGAG ATGNGGNCG GGACATAGTG	60
GTACACANCT GTAATGCTCA NCACTKATGG GGAGTACTGA AGGNGGNSSG ATCACTTGNG	120
GGTCNGGAAT NTGAGANCAG CCTGGCAAN ATGGCGAAC CCTGTCTCTA CTAAAATAG	180
CCANAAWNWA GCCTAGCGTG GTGGCGCRCA CGCGTGGTTC CACCTACTCA GGAGGCNTAA	240
GCACGAGNAN TNCTTGAACC CAGGAGGCAG AGGNTGTGGT GARCTGAGAT CGTGCCTAG	300
CACTCCAGTC TGGGCGACMA AGTGAGACCC TGTCTCCNNN AAGAAAAAAA AAATCTGTAC	360
TTTTTAAGGG TTGTGGGACC TGTAAATTAT ATTGAAATGC TTCTYTTCTA GGTCATCCAT	420
GCCTGGCTTA TTATATCATC TCTATTGTTG CTGCTCTTT TTACATTCTAT TTACTTGGGG	480
TAAGTTGTGA AATTTGGGGT CTGTCTTTCA GAATTAACCA CCTNNNGTGT GTGTAGCTAT	540
CATTTAAAGC CATGTACTTT GNTGATGAAT TACTCTGAAG TTTTAATTGT NTCCACATAT	600
AGGTCAACT TGGTATATAA AAGACTAGNC AGTATTACTA ATTGAGACAT TCTTCTGTNG	660
CTCCTNGCTT ATAATAAGTA GAACTGAAAG NAACCTAAGA CTACAGTTAA TTCTAAGCCT	720
TTGGGGAAGG ATTATATAGC CTTCTAGTAG GAAGTCTTGT GCNATCAGAA TGTTNTAAA	780
GAAAGGGTNT CAAGGAATNG TATAANACC AAAAATAATT GAT	823

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

GTNTCCNAACCAACTTAGG AGNTTGGACC TGGGRAAGAC CNACNTGATC TCCGGGAGGN	60
AAAGACTNCA GTTGAGCCGT GATTGCACCC ACTTTACTCC AAGCCTGGGC AACCAAAATG	120

AGACACTGGC	TCCAAACACA	AAAACAAAAA	CAAAAAAAGA	GTAAATTAAT	TTANAGGGAA	180
GNATTAAATA	AATAATAGCA	CAGTTGATAT	AGGTTATGGT	AAAATTATAA	AGGTGGGANA	240
TTAATATCTA	ATGTTGGGA	GCCATCACAT	TATTCTAAAT	AATGTTTGG	TGGAAATTAT	300
TGTACATCTT	TTAAAATCTG	TGTAATTTTT	TTTCAGGGAA	GTGTTAAAA	CCTATAACGT	360
TGCTGTGGAC	TACATTACTG	TTNCACTCCT	GATCTGGAAT	TTTGGTGTGG	TGGGAATGAT	420
TTCCATTAC	TGGAAAGGTC	CACTTCGACT	CCAGCAGGCA	TATCTCATTA	TGATTAGTGC	480
CCTCATGNCC	CTGKTGTTA	TCAAGTACCT	CCCTGAATGG	ACTGNGTGGC	TCATCTTGGC	540
TGTGATTCA	GTATATGGTA	AAACCCAAGA	CTGATAATTT	TTTGTACACA	GGAATGCC	600
ACTGGAGTGT	TTTCTTCCT	CATCTCTTA	TCTTGATTAA	GAGAAAATGG	TAACGTGTAC	660
ATCCCATAAC	TCTTCAGTAA	ATCATTAAATT	AGCTATAGTA	ACTTTTCAT	TTGAAGATT	720
CGGCTGGCA	TGGTAGCTA	TGCCTGTAAT	CTTAGCACTT	TGGGAGGCTG	AGGCAGGCAG	780
ATCACCTAAG	CCCAGAGTTC	AAGACCAGCC	TGGGCAACAT	GGCAAAACCT	CGTATCTACA	840
GAAAATACAA	AAATTAGCCG	GGCATGGTGG	TGCACACCTG	TAGTTCCAGC	TACTTAGGAG	900
GCTGAGGTGG	GAGGATCGAT	TGATCCCAGG	AGGTCAAGNC	TGCAG		945